

C 253	21	0.3	24	1	AZ404871	ACCESSION:AZ404871	326	20.4	0.3	22	1	CF310366	ACCESSION:CF310366
C 254	21	0.3	24	1	AZ786257	ACCESSION:AZ786257	327	20.4	0.3	22	1	CF311269	ACCESSION:CF311269
255	21	0.3	25	1	N27663	ACCESSION:N27663	C 328	20.4	0.3	22	1	CF311713	ACCESSION:CF311713
256	21	0.3	25	1	CG726337	ACCESSION:CG726337	C 329	20.4	0.3	22	1	CF312498	ACCESSION:CF312498
C 257	21	0.3	26	1	CF280688	ACCESSION:CF280688	330	20.4	0.3	22	1	CF330679	ACCESSION:CF330679
C 258	21	0.3	27	1	CF310745	ACCESSION:CF310745	331	20.4	0.3	22	1	CF333430	ACCESSION:CF333430
259	21	0.3	29	1	CF295451	ACCESSION:CF295451	332	20.4	0.3	22	1	CF334781	ACCESSION:CF334781
260	21	0.3	29	1	CF299155	ACCESSION:CF299155	333	20.4	0.3	22	1	CF336250	ACCESSION:CF336250
261	21	0.3	29	1	CF314795	ACCESSION:CF314795	C 334	20.4	0.3	22	1	CF337580	ACCESSION:CF337580
262	21	0.3	30	1	BQ592535	ACCESSION:BQ592535	C 335	20.4	0.3	22	1	CF338524	ACCESSION:CF338524
C 263	21	0.3	30	1	TA226050P	ACCESSION:TA226050P	336	20.4	0.3	22	1	A2310066	ACCESSION:A2310066
264	21	0.3	31	1	CF311684	ACCESSION:CF311684	C 337	20.4	0.3	22	1	A2351527	ACCESSION:A2351527
265	21	0.3	31	1	CF312635	ACCESSION:CF312635	C 338	20.4	0.3	22	1	A2357630	ACCESSION:A2357630
266	21	0.3	32	1	AV675687	ACCESSION:AV675687	C 339	20.4	0.3	22	1	A2374487	ACCESSION:A2374487
267	21	0.3	32	1	AV965254	ACCESSION:AV965254	C 340	20.4	0.3	22	1	A2388103	ACCESSION:A2388103
268	21	0.3	32	1	AV965452	ACCESSION:AV965452	341	20.4	0.3	22	1	A2401908	ACCESSION:A2401908
269	21	0.3	32	1	BX551100	ACCESSION:BX551100	342	20.4	0.3	22	1	A2424307	ACCESSION:A2424307
270	21	0.3	32	1	BX555625	ACCESSION:BX555625	343	20.4	0.3	22	1	A2428818	ACCESSION:A2428818
C 271	21	0.3	32	1	BX557354	ACCESSION:BX557354	344	20.4	0.3	22	1	A2459654	ACCESSION:A2459654
C 272	20.8	0.3	24	1	BG670391	ACCESSION:BG670391	345	20.4	0.3	22	1	A2463503	ACCESSION:A2463503
273	20.8	0.3	24	1	BX554611	ACCESSION:BX554611	346	20.4	0.3	22	1	A2463652	ACCESSION:A2463652
274	20.8	0.3	24	1	CA853764	ACCESSION:CA853764	347	20.4	0.3	22	1	A2582403	ACCESSION:A2582403
C 275	20.8	0.3	24	1	CF276855	ACCESSION:CF276855	C 348	20.4	0.3	22	1	A2607658	ACCESSION:A2607658
276	20.8	0.3	24	1	CF301361	ACCESSION:CF301361	C 349	20.4	0.3	22	1	A2654691	ACCESSION:A2654691
277	20.8	0.3	24	1	CF312319	ACCESSION:CF312319	C 350	20.4	0.3	22	1	A2760533	ACCESSION:A2760533
C 278	20.8	0.3	24	1	CF320862	ACCESSION:CF320862	351	20.4	0.3	22	1	A2779844	ACCESSION:A2779844
279	20.8	0.3	24	1	A2328848	ACCESSION:A2328848	352	20.4	0.3	22	1	A2785019	ACCESSION:A2785019
C 280	20.8	0.3	24	1	A2363562	ACCESSION:A2363562	353	20.4	0.3	22	1	A2787098	ACCESSION:A2787098
C 281	20.8	0.3	24	1	A2386491	ACCESSION:A2386491	354	20.4	0.3	22	1	A2787606	ACCESSION:A2787606
C 282	20.8	0.3	24	1	A2390642	ACCESSION:A2390642	355	20.4	0.3	22	1	A2792704	ACCESSION:A2792704
283	20.8	0.3	24	1	A2459280	ACCESSION:A2459280	356	20.4	0.3	22	1	A2810674	ACCESSION:A2810674
284	20.8	0.3	24	1	A2644621	ACCESSION:A2644621	357	20.4	0.3	22	1	A2820439	ACCESSION:A2820439
C 285	20.8	0.3	24	1	A2834990	ACCESSION:A2834990	C 358	20.4	0.3	22	1	A2841661	ACCESSION:A2841661
C 286	20.8	0.3	24	1	A2970038	ACCESSION:A2970038	359	20.4	0.3	22	1	A2843514	ACCESSION:A2843514
C 287	20.8	0.3	24	1	A2984490	ACCESSION:A2984490	C 360	20.4	0.3	22	1	A2946102	ACCESSION:A2946102
C 288	20.8	0.3	24	1	A2993423	ACCESSION:A2993423	C 361	20.4	0.3	22	1	TA131B09P	ACCESSION:TA131B09P
289	20.8	0.3	24	1	TA169D12P	ACCESSION:TA169D12P	C 362	20.4	0.3	22	1	TA329F10P	ACCESSION:TA329F10P
C 290	20.8	0.3	24	1	TA27B08Q	ACCESSION:TA27B08Q	363	20.4	0.3	22	1	TA35C12Q	ACCESSION:TA35C12Q
C 291	20.8	0.3	24	1	TA354C06P	ACCESSION:TA354C06P	C 364	20.4	0.3	22	1	TA380A07P	ACCESSION:TA380A07P
C 292	20.8	0.3	24	1	TA371F11P	ACCESSION:TA371F11P	C 365	20.4	0.3	23	1	AL048745	ACCESSION:AL048745
C 293	20.8	0.3	24	1	TA95B08P	ACCESSION:TA95B08P	366	20.4	0.3	23	1	CF279238	ACCESSION:CF279238
294	20.8	0.3	25	1	AL587648	ACCESSION:AL587648	367	20.4	0.3	23	1	CF297943	ACCESSION:CF297943
C 295	20.8	0.3	25	1	N33150	ACCESSION:N33150	C 368	20.4	0.3	23	1	CF310501	ACCESSION:CF310501
C 296	20.8	0.3	25	1	A2381039	ACCESSION:A2381039	369	20.4	0.3	23	1	CF319212	ACCESSION:CF319212
C 297	20.8	0.3	25	1	A2386891	ACCESSION:A2386891	C 370	20.4	0.3	23	1	CF322953	ACCESSION:CF322953
298	20.8	0.3	25	1	TA154D03P	ACCESSION:TA154D03P	C 371	20.4	0.3	23	1	CF329042	ACCESSION:CF329042
299	20.8	0.3	26	1	CF336199	ACCESSION:CF336199	C 372	20.4	0.3	23	1	CF334657	ACCESSION:CF334657
C 300	20.8	0.3	27	1	CF639306	ACCESSION:CF639306	373	20.4	0.3	23	1	A2309219	ACCESSION:A2309219
C 301	20.8	0.3	27	1	TA257B07P	ACCESSION:TA257B07P	C 374	20.4	0.3	23	1	A2309851	ACCESSION:A2309851
302	20.8	0.3	28	1	AU257468	ACCESSION:AU257468	375	20.4	0.3	23	1	A2312314	ACCESSION:A2312314
303	20.8	0.3	28	1	CF277114	ACCESSION:CF277114	376	20.4	0.3	23	1	A2313922	ACCESSION:A2313922
C 304	20.8	0.3	28	1	CF299294	ACCESSION:CF299294	C 377	20.4	0.3	23	1	A2351354	ACCESSION:A2351354
305	20.8	0.3	28	1	TS6352	ACCESSION:TS6352	C 378	20.4	0.3	23	1	A2357645	ACCESSION:A2357645
306	20.8	0.3	29	1	BX568640	ACCESSION:BX568640	C 379	20.4	0.3	23	1	A2419236	ACCESSION:A2419236
C 307	20.8	0.3	29	1	CF328476	ACCESSION:CF328476	C 380	20.4	0.3	23	1	A2465327	ACCESSION:A2465327
C 308	20.8	0.3	30	1	DR31A15T	ACCESSION:DR31A15T	381	20.4	0.3	23	1	A2481702	ACCESSION:A2481702
309	20.8	0.3	30	1	TA247F06P	ACCESSION:TA247F06P	382	20.4	0.3	23	1	A2588254	ACCESSION:A2588254
C 310	20.8	0.3	31	1	A2435988	ACCESSION:A2435988	383	20.4	0.3	23	1	A2593540	ACCESSION:A2593540
C 311	20.8	0.3	32	1	AV958999	ACCESSION:AV958999	384	20.4	0.3	23	1	A2610785	ACCESSION:A2610785
C 312	20.8	0.3	32	1	CF296152	ACCESSION:CF296152	C 385	20.4	0.3	23	1	A2621676	ACCESSION:A2621676
313	20.8	0.3	32	1	A2345558	ACCESSION:A2345558	C 386	20.4	0.3	23	1	A2647637	ACCESSION:A2647637
314	20.8	0.3	32	1	CG707472	ACCESSION:CG707472	387	20.4	0.3	23	1	A2654903	ACCESSION:A2654903
315	20.6	0.3	28	1	CF334115	ACCESSION:CF334115	C 388	20.4	0.3	23	1	A2778751	ACCESSION:A2778751
316	20.6	0.3	29	1	CF300706	ACCESSION:CF300706	C 389	20.4	0.3	23	1	A2787184	ACCESSION:A2787184
317	20.6	0.3	29	1	CF330960	ACCESSION:CF330960	C 390	20.4	0.3	23	1	A2792751	ACCESSION:A2792751
318	20.6	0.3	30	1	BX555986	ACCESSION:BX555986	391	20.4	0.3	23	1	AZ801003	ACCESSION:AZ801003
319	20.6	0.3	30	1	BX554037	ACCESSION:BX554037	C 392	20.4	0.3	23	1	AZ817623	ACCESSION:AZ817623
320	20.6	0.3	31	1	BX554615	ACCESSION:BX554615	C 393	20.4	0.3	23	1	AZ859570	ACCESSION:AZ859570
321	20.6	0.3	31	1	BX556269	ACCESSION:BX556269	C 394	20.4	0.3	23	1	AZ939608	ACCESSION:AZ939608
322	20.4	0.3	22	1	AW332181	ACCESSION:AW332181	C 395	20.4	0.3	23	1	BH000534	ACCESSION:BH000534
323	20.4	0.3	22	1	AW332399	ACCESSION:AW332399	C 396	20.4	0.3	23	1	TA151C03Q	ACCESSION:TA151C03Q
324	20.4	0.3	22	1	CF299342	ACCESSION:CF299342	C 397	20.4	0.3	23	1	TA274B03P	ACCESSION:TA274B03P
325	20.4	0.3	22	1	CF300133	ACCESSION:CF300133	398	20.4	0.3	23	1		

C 399	20.4	0.3	23	1	TA353A10P	ACCESSION: AL494456	472	20	0.3	20	1	T50579	ACCESSION: T50579
C 400	20.4	0.3	24	1	AZ438069	ACCESSION: AZ438069	473	20	0.3	20	1	AZ307671	ACCESSION: AZ307671
C 401	20.4	0.3	25	1	CF317007	ACCESSION: CF317007	474	20	0.3	20	1	AZ333980	ACCESSION: AZ333980
C 402	20.4	0.3	26	1	CF296646	ACCESSION: CF296646	C 475	20	0.3	20	1	AZ341530	ACCESSION: AZ341530
C 403	20.4	0.3	26	1	R26779	ACCESSION: R26779	C 476	20	0.3	20	1	AZ343031	ACCESSION: AZ343031
C 404	20.4	0.3	26	1	CNS00BGV	ACCESSION: AL057060	C 477	20	0.3	20	1	AZ345856	ACCESSION: AZ345856
C 405	20.4	0.3	26	1	TA321G11P	ACCESSION: AL492371	C 478	20	0.3	20	1	AZ351273	ACCESSION: AZ351273
C 406	20.4	0.3	27	1	N34459	ACCESSION: N34459	C 479	20	0.3	20	1	AZ357623	ACCESSION: AZ357623
C 407	20.4	0.3	27	1	T52979	ACCESSION: T52979	C 480	20	0.3	20	1	AZ369734	ACCESSION: AZ369734
C 408	20.4	0.3	27	1	AZ812708	ACCESSION: AZ812708	C 481	20	0.3	20	1	AZ386573	ACCESSION: AZ386573
C 409	20.4	0.3	28	1	AZ357605	ACCESSION: AZ357605	C 482	20	0.3	20	1	AZ396481	ACCESSION: AZ396481
C 410	20.4	0.3	29	1	AL048747	ACCESSION: AL048747	C 483	20	0.3	20	1	AZ442328	ACCESSION: AZ442328
C 411	20.4	0.3	29	1	BQ586486	ACCESSION: BQ586486	C 484	20	0.3	20	1	AZ463331	ACCESSION: AZ463331
C 412	20.4	0.3	29	1	BX567540	ACCESSION: BX567540	485	20	0.3	20	1	AZ477734	ACCESSION: AZ477734
C 413	20.4	0.3	29	1	BX627582	ACCESSION: BX627582	486	20	0.3	20	1	AZ479464	ACCESSION: AZ479464
C 414	20.4	0.3	29	1	CF312595	ACCESSION: CF312595	487	20	0.3	20	1	AZ498625	ACCESSION: AZ498625
C 415	20.4	0.3	29	1	AZ825156	ACCESSION: AZ825156	C 488	20	0.3	20	1	AZ514729	ACCESSION: AZ514729
C 416	20.4	0.3	29	1	TA378G07P	ACCESSION: AL497621	C 489	20	0.3	20	1	AZ579178	ACCESSION: AZ579178
C 417	20.4	0.3	30	1	BE539470	ACCESSION: BE539470	C 490	20	0.3	20	1	AZ581208	ACCESSION: AZ581208
C 418	20.4	0.3	30	1	BM280395	ACCESSION: BM280395	C 491	20	0.3	20	1	AZ588011	ACCESSION: AZ588011
C 419	20.4	0.3	30	1	BX549675	ACCESSION: BX549675	C 492	20	0.3	20	1	AZ607328	ACCESSION: AZ607328
C 420	20.4	0.3	30	1	BX551003	ACCESSION: BX551003	C 493	20	0.3	20	1	AZ623155	ACCESSION: AZ623155
C 421	20.4	0.3	30	1	BX554779	ACCESSION: BX554779	C 494	20	0.3	20	1	AZ623214	ACCESSION: AZ623214
C 422	20.4	0.3	30	1	BX555710	ACCESSION: BX555710	C 495	20	0.3	20	1	AZ643992	ACCESSION: AZ643992
C 423	20.4	0.3	30	1	BX559425	ACCESSION: BX559425	496	20	0.3	20	1	AZ645829	ACCESSION: AZ645829
C 424	20.4	0.3	30	1	BX563547	ACCESSION: BX563547	C 497	20	0.3	20	1	AZ650271	ACCESSION: AZ650271
C 425	20.4	0.3	30	1	BX565972	ACCESSION: BX565972	C 498	20	0.3	20	1	AZ760838	ACCESSION: AZ760838
C 426	20.4	0.3	31	1	AW245279	ACCESSION: AW245279	C 499	20	0.3	20	1	AZ764504	ACCESSION: AZ764504
C 427	20.4	0.3	31	1	BX554068	ACCESSION: BX554068	500	20	0.3	20	1	AZ765211	ACCESSION: AZ765211
C 428	20.4	0.3	31	1	BX557470	ACCESSION: BX557470	C 501	20	0.3	20	1	AZ772091	ACCESSION: AZ772091
C 429	20.4	0.3	31	1	BX558479	ACCESSION: BX558479	502	20	0.3	20	1	AZ779425	ACCESSION: AZ779425
C 430	20.4	0.3	31	1	BX559254	ACCESSION: BX559254	C 503	20	0.3	20	1	AZ784041	ACCESSION: AZ784041
C 431	20.4	0.3	32	1	CF296152	ACCESSION: CF296152	504	20	0.3	20	1	AZ793467	ACCESSION: AZ793467
C 432	20.2	0.3	25	1	AU265663	ACCESSION: AU265663	505	20	0.3	20	1	AZ798529	ACCESSION: AZ798529
C 433	20.2	0.3	25	1	CF317378	ACCESSION: CF317378	C 506	20	0.3	20	1	AZ805163	ACCESSION: AZ805163
C 434	20.2	0.3	25	1	AZ404078	ACCESSION: AZ404078	C 507	20	0.3	20	1	AZ806521	ACCESSION: AZ806521
C 435	20.2	0.3	26	1	AZ316353	ACCESSION: AZ316353	C 508	20	0.3	20	1	AZ806585	ACCESSION: AZ806585
C 436	20.2	0.3	26	1	AZ355083	ACCESSION: AZ355083	C 509	20	0.3	20	1	AZ809306	ACCESSION: AZ809306
C 437	20.2	0.3	26	1	AZ623156	ACCESSION: AZ623156	C 510	20	0.3	20	1	AZ810986	ACCESSION: AZ810986
C 438	20.2	0.3	26	1	AZ635695	ACCESSION: AZ635695	C 511	20	0.3	20	1	AZ813908	ACCESSION: AZ813908
C 439	20.2	0.3	27	1	CF298133	ACCESSION: CF298133	C 512	20	0.3	20	1	AZ817323	ACCESSION: AZ817323
C 440	20.2	0.3	27	1	AZ434285	ACCESSION: AZ434285	C 513	20	0.3	20	1	AZ817414	ACCESSION: AZ817414
C 441	20.2	0.3	27	1	AL582228	ACCESSION: AL582228	C 514	20	0.3	20	1	AZ817467	ACCESSION: AZ817467
C 442	20.2	0.3	28	1	AL587605	ACCESSION: AL587605	515	20	0.3	20	1	AZ817608	ACCESSION: AZ817608
C 443	20.2	0.3	28	1	AW332443	ACCESSION: AW332443	516	20	0.3	20	1	AZ818489	ACCESSION: AZ818489
C 444	20.2	0.3	28	1	CF307749	ACCESSION: CF307749	517	20	0.3	20	1	AZ818816	ACCESSION: AZ818816
C 445	20.2	0.3	28	1	AZ836072	ACCESSION: AZ836072	C 518	20	0.3	20	1	AZ837491	ACCESSION: AZ837491
C 446	20.2	0.3	28	1	TA29A09P	ACCESSION: AL453073	C 519	20	0.3	20	1	AZ841342	ACCESSION: AZ841342
C 447	20.2	0.3	29	1	BQ583967	ACCESSION: BQ583967	520	20	0.3	20	1	AZ841558	ACCESSION: AZ841558
C 448	20.2	0.3	29	1	AZ827060	ACCESSION: AZ827060	C 521	20	0.3	20	1	AZ858052	ACCESSION: AZ858052
C 449	20.2	0.3	30	1	BX659426	ACCESSION: BX659426	C 522	20	0.3	20	1	AZ858614	ACCESSION: AZ858614
C 450	20.2	0.3	31	1	AU268044	ACCESSION: AU268044	523	20	0.3	20	1	AZ949180	ACCESSION: AZ949180
C 451	20.2	0.3	31	1	BQ591372	ACCESSION: BQ591372	524	20	0.3	20	1	AZ963973	ACCESSION: AZ963973
C 452	20.2	0.3	31	1	CF297930	ACCESSION: CF297930	C 525	20	0.3	21	1	AL048777	ACCESSION: AL048777
C 453	20.2	0.3	31	1	AZ486763	ACCESSION: AZ486763	526	20	0.3	21	1	BX556006	ACCESSION: BX556006
C 454	20.2	0.3	31	1	AZ785111	ACCESSION: AZ785111	527	20	0.3	21	1	BX558161	ACCESSION: BX558161
C 455	20	0.3	20	1	AW334823	ACCESSION: AW334823	528	20	0.3	21	1	CF276638	ACCESSION: CF276638
C 456	20	0.3	20	1	CF280913	ACCESSION: CF280913	C 529	20	0.3	21	1	CF282216	ACCESSION: CF282216
C 457	20	0.3	20	1	CF282035	ACCESSION: CF282035	530	20	0.3	21	1	CF292703	ACCESSION: CF292703
C 458	20	0.3	20	1	CF282414	ACCESSION: CF282414	531	20	0.3	21	1	CF295642	ACCESSION: CF295642
C 459	20	0.3	20	1	CF299822	ACCESSION: CF299822	C 532	20	0.3	21	1	CF297615	ACCESSION: CF297615
C 460	20	0.3	20	1	CF301720	ACCESSION: CF301720	533	20	0.3	21	1	CF308322	ACCESSION: CF308322
C 461	20	0.3	20	1	CF302027	ACCESSION: CF302027	534	20	0.3	21	1	CF300809	ACCESSION: CF300809
C 462	20	0.3	20	1	CF310604	ACCESSION: CF310604	C 535	20	0.3	21	1	CF312715	ACCESSION: CF312715
C 463	20	0.3	20	1	CF313067	ACCESSION: CF313067	536	20	0.3	21	1	CF316073	ACCESSION: CF316073
C 464	20	0.3	20	1	CF313569	ACCESSION: CF313569	537	20	0.3	21	1	CF326952	ACCESSION: CF326952
C 465	20	0.3	20	1	CF319133	ACCESSION: CF319133	C 538	20	0.3	21	1	CF327391	ACCESSION: CF327391
C 466	20	0.3	20	1	CF321721	ACCESSION: CF321721	539	20	0.3	21	1	CF332956	ACCESSION: CF332956
C 467	20	0.3	20	1	CF328565	ACCESSION: CF328565	C 540	20	0.3	21	1	CF338057	ACCESSION: CF338057
C 468	20	0.3	20	1	CF333173	ACCESSION: CF333173	541	20	0.3	21	1	CF338522	ACCESSION: CF338522
C 469	20	0.3	20	1	CF334170	ACCESSION: CF334170	C 542	20	0.3	21	1	AZ348593	ACCESSION: AZ348593
C 470	20	0.3	20	1	CF336525	ACCESSION: CF336525	C 543	20	0.3	21	1	AZ350611	ACCESSION: AZ350611
C 471	20	0.3	20	1	CF337494	ACCESSION: CF337494	C 544	20	0.3	21	1	AZ386711	ACCESSION: AZ386711



C 691	19	0.3	19	1	AZ307313	ACCSSION:AZ307313	C 764	19	0.3	22	1	TA231E08Q	ACCSSION:AL480935
C 692	19	0.3	19	1	AZ310079	ACCSSION:AZ310079	C 765	19	0.3	26	1	CF318508	ACCSSION:CF318508
C 693	19	0.3	19	1	AZ310105	ACCSSION:AZ310105	C 766	19	0.3	26	1	TA236D08P	ACCSSION:AL482943
C 694	19	0.3	19	1	AZ317743	ACCSSION:AZ317743	C 767	19	0.3	27	1	BI094728	ACCSSION:BI094728
C 695	19	0.3	19	1	AZ340311	ACCSSION:AZ340311	C 768	19	0.3	27	1	CF311022	ACCSSION:CF311022
C 696	19	0.3	19	1	AZ350519	ACCSSION:AZ350519	C 769	19	0.3	27	1	N51845	ACCSSION:N51845
C 697	19	0.3	19	1	AZ364226	ACCSSION:AZ364226	C 770	19	0.3	27	1	TA386G03Q	ACCSSION:AL498287
C 698	19	0.3	19	1	AZ356696	ACCSSION:AZ356696	C 771	19	0.3	28	1	AI971979	ACCSSION:AI971979
C 699	19	0.3	19	1	AZ374409	ACCSSION:AZ374409	C 772	19	0.3	28	1	AZ803177	ACCSSION:AZ803177
C 700	19	0.3	19	1	AZ374619	ACCSSION:AZ374619	C 773	19	0.3	28	1	TA173D10P	ACCSSION:AL473898
C 701	19	0.3	19	1	AZ385952	ACCSSION:AZ385952	C 774	19	0.3	28	1	TA327D04P	ACCSSION:AL497297
C 702	19	0.3	19	1	AZ391509	ACCSSION:AZ391509	C 775	19	0.3	29	1	CF290997	ACCSSION:CF290997
C 703	19	0.3	19	1	AZ410050	ACCSSION:AZ410050	C 776	19	0.3	29	1	CF310757	ACCSSION:CF310757
C 704	19	0.3	19	1	AZ414413	ACCSSION:AZ414413	C 777	18.8	0.3	22	1	CF298427	ACCSSION:CF298427
C 705	19	0.3	19	1	AZ422604	ACCSSION:AZ422604	C 778	18.8	0.3	22	1	TA303G05P	ACCSSION:AL497383
C 706	19	0.3	19	1	AZ424716	ACCSSION:AZ424716	C 779	18.8	0.3	23	1	AX568055	ACCSSION:AX568055
C 707	19	0.3	19	1	AZ441329	ACCSSION:AZ441329	C 780	18.8	0.3	23	1	CF290997	ACCSSION:CF290997
C 708	19	0.3	19	1	AZ442365	ACCSSION:AZ442365	C 781	18.8	0.3	23	1	CF311534	ACCSSION:CF311534
C 709	19	0.3	19	1	AZ453930	ACCSSION:AZ453930	C 782	18.8	0.3	23	1	AZ382013	ACCSSION:AZ382013
C 710	19	0.3	19	1	AZ460906	ACCSSION:AZ460906	C 783	18.8	0.3	23	1	AZ486853	ACCSSION:AZ486853
C 711	19	0.3	19	1	AZ471494	ACCSSION:AZ471494	C 784	18.8	0.3	23	1	AZ627841	ACCSSION:AZ627841
C 712	19	0.3	19	1	AZ476576	ACCSSION:AZ476576	C 785	18.8	0.3	23	1	AZ645254	ACCSSION:AZ645254
C 713	19	0.3	19	1	AZ486786	ACCSSION:AZ486786	C 786	18.8	0.3	23	1	TA55C06P	ACCSSION:AL455778
C 714	19	0.3	19	1	AZ490652	ACCSSION:AZ490652	C 787	18.8	0.3	25	1	AZ867155	ACCSSION:AZ867155
C 715	19	0.3	19	1	AZ508040	ACCSSION:AZ508040	C 788	18.8	0.3	25	1	AX555323	ACCSSION:AX555323
C 716	19	0.3	19	1	AZ579119	ACCSSION:AZ579119	C 789	18.8	0.3	30	1	TA247E06P	ACCSSION:AL483252
C 717	19	0.3	19	1	AZ583970	ACCSSION:AZ583970	C 790	18.6	0.2	25	1	AX512788	ACCSSION:AX512788
C 718	19	0.3	19	1	AZ585865	ACCSSION:AZ585865	C 791	18.6	0.2	25	1	AW249476	ACCSSION:AW249476
C 719	19	0.3	19	1	AZ593210	ACCSSION:AZ593210	C 792	18.6	0.2	25	1	CF319953	ACCSSION:CF319953
C 720	19	0.3	19	1	AZ616154	ACCSSION:AZ616154	C 793	18.6	0.2	25	1	AZ442170	ACCSSION:AZ442170
C 721	19	0.3	19	1	AZ627844	ACCSSION:AZ627844	C 794	18.6	0.2	25	1	AZ476141	ACCSSION:AZ476141
C 722	19	0.3	19	1	AZ631701	ACCSSION:AZ631701	C 795	18.6	0.2	25	1	BZ765670	ACCSSION:BZ765670
C 723	19	0.3	19	1	AZ633821	ACCSSION:AZ633821	C 796	18.6	0.2	26	1	BM658913	ACCSSION:BM658913
C 724	19	0.3	19	1	AZ643659	ACCSSION:AZ643659	C 797	18.6	0.2	26	1	AX563414	ACCSSION:AX563414
C 725	19	0.3	19	1	AZ644698	ACCSSION:AZ644698	C 798	18.6	0.2	26	1	CF337311	ACCSSION:CF337311
C 726	19	0.3	19	1	AZ648335	ACCSSION:AZ648335	C 799	18.6	0.2	26	1	AZ437459	ACCSSION:AZ437459
C 727	19	0.3	19	1	AZ649888	ACCSSION:AZ649888	C 800	18.6	0.2	26	1	AZ771474	ACCSSION:AZ771474
C 728	19	0.3	19	1	AZ764497	ACCSSION:AZ764497	C 801	18.6	0.2	26	1	BZ593276	ACCSSION:BZ593276
C 729	19	0.3	19	1	AZ764522	ACCSSION:AZ764522	C 802	18.6	0.2	27	1	CF318113	ACCSSION:CF318113
C 730	19	0.3	19	1	AZ764534	ACCSSION:AZ764534	C 803	18.6	0.2	27	1	AZ495352	ACCSSION:AZ495352
C 731	19	0.3	19	1	AZ770387	ACCSSION:AZ770387	C 804	18.6	0.2	28	1	AX335064	ACCSSION:AX335064
C 732	19	0.3	19	1	AZ778858	ACCSSION:AZ778858	C 805	18.6	0.2	28	1	AX549093	ACCSSION:AX549093
C 733	19	0.3	19	1	AZ779901	ACCSSION:AZ779901	C 806	18.6	0.2	28	1	AX549709	ACCSSION:AX549709
C 734	19	0.3	19	1	AZ781876	ACCSSION:AZ781876	C 807	18.6	0.2	28	1	AX551130	ACCSSION:AX551130
C 735	19	0.3	19	1	AZ787634	ACCSSION:AZ787634	C 808	18.6	0.2	28	1	AX551489	ACCSSION:AX551489
C 736	19	0.3	19	1	AZ788058	ACCSSION:AZ788058	C 809	18.6	0.2	28	1	AX551507	ACCSSION:AX551507
C 737	19	0.3	19	1	AZ789590	ACCSSION:AZ789590	C 810	18.6	0.2	28	1	AX551765	ACCSSION:AX551765
C 738	19	0.3	19	1	AZ792713	ACCSSION:AZ792713	C 811	18.6	0.2	28	1	AX551818	ACCSSION:AX551818
C 739	19	0.3	19	1	AZ795403	ACCSSION:AZ795403	C 812	18.6	0.2	28	1	AX552134	ACCSSION:AX552134
C 740	19	0.3	19	1	AZ801970	ACCSSION:AZ801970	C 813	18.6	0.2	28	1	AX553072	ACCSSION:AX553072
C 741	19	0.3	19	1	AZ822225	ACCSSION:AZ822225	C 814	18.6	0.2	28	1	AX553346	ACCSSION:AX553346
C 742	19	0.3	19	1	AZ841581	ACCSSION:AZ841581	C 815	18.6	0.2	28	1	AX553393	ACCSSION:AX553393
C 743	19	0.3	19	1	AZ841622	ACCSSION:AZ841622	C 816	18.6	0.2	28	1	AX553451	ACCSSION:AX553451
C 744	19	0.3	19	1	AZ861896	ACCSSION:AZ861896	C 817	18.6	0.2	28	1	AX553531	ACCSSION:AX553531
C 745	19	0.3	19	1	AZ936798	ACCSSION:AZ936798	C 818	18.6	0.2	28	1	AX553626	ACCSSION:AX553626
C 746	19	0.3	19	1	AZ985501	ACCSSION:AZ985501	C 819	18.6	0.2	28	1	AX553647	ACCSSION:AX553647
C 747	19	0.3	19	1	BH000498	ACCSSION:BH000498	C 820	18.6	0.2	28	1	AX554302	ACCSSION:AX554302
C 748	19	0.3	20	1	AL587572	ACCSSION:AL587572	C 821	18.6	0.2	28	1	AX554631	ACCSSION:AX554631
C 749	19	0.3	20	1	CF282002	ACCSSION:CF282002	C 822	18.6	0.2	28	1	AX555415	ACCSSION:AX555415
C 750	19	0.3	20	1	CF316662	ACCSSION:CF316662	C 823	18.6	0.2	28	1	AX555424	ACCSSION:AX555424
C 751	19	0.3	20	1	CF318278	ACCSSION:CF318278	C 824	18.6	0.2	28	1	AX555683	ACCSSION:AX555683
C 752	19	0.3	20	1	CF320843	ACCSSION:CF320843	C 825	18.6	0.2	28	1	AX555705	ACCSSION:AX555705
C 753	19	0.3	20	1	AZ341237	ACCSSION:AZ341237	C 826	18.6	0.2	28	1	AX555861	ACCSSION:AX555861
C 754	19	0.3	20	1	AZ486784	ACCSSION:AZ486784	C 827	18.6	0.2	28	1	AX556242	ACCSSION:AX556242
C 755	19	0.3	20	1	AZ638704	ACCSSION:AZ638704	C 828	18.6	0.2	28	1	AX556265	ACCSSION:AX556265
C 756	19	0.3	20	1	AZ821905	ACCSSION:AZ821905	C 829	18.6	0.2	28	1	AX556442	ACCSSION:AX556442
C 757	19	0.3	20	1	AZ858419	ACCSSION:AZ858419	C 830	18.6	0.2	28	1	AX556491	ACCSSION:AX556491
C 758	19	0.3	20	1	AL587702	ACCSSION:AL587702	C 831	18.6	0.2	28	1	AX556540	ACCSSION:AX556540
C 759	19	0.3	21	1	CF302218	ACCSSION:CF302218	C 832	18.6	0.2	28	1	AX556549	ACCSSION:AX556549
C 760	19	0.3	21	1	CF314260	ACCSSION:CF314260	C 833	18.6	0.2	28	1	AX556602	ACCSSION:AX556602
C 761	19	0.3	21	1	CF310486	ACCSSION:CF310486	C 834	18.6	0.2	28	1	AX557090	ACCSSION:AX557090
C 762	19	0.3	22	1	AZ309907	ACCSSION:AZ309907	C 835	18.6	0.2	28	1	AX557380	ACCSSION:AX557380
C 763	19	0.3	22	1	AZ309907	ACCSSION:AZ309907	C 836	18.6	0.2	28	1	AX557739	ACCSSION:AX557739





983	17.6	0.2	27	1	BX560901	ACCESSION:BX560901	c1056	17	0.2	21	1	AZ764492	ACCESSION:AZ764492
984	17.6	0.2	27	1	BX562177	ACCESSION:BX562177	1057	17	0.2	22	1	CF310806	ACCESSION:CF310806
985	17.6	0.2	27	1	BX564083	ACCESSION:BX564083	1058	17	0.2	22	1	AZ310057	ACCESSION:AZ310057
986	17.6	0.2	27	1	CF328811	ACCESSION:CF328811	1059	17	0.2	23	1	BX550903	ACCESSION:BX550903
987	17.6	0.2	27	1	AZ953355	ACCESSION:AZ953355	c1060	17	0.2	24	1	AZ448207	ACCESSION:AZ448207
988	17.6	0.2	27	1	TA165H05P	ACCESSION:AL472045	c1061	17	0.2	25	1	AU268810	ACCESSION:AU268810
989	17.4	0.2	19	1	AW248747	ACCESSION:AW248747	1062	17	0.2	25	1	AW245275	ACCESSION:AW245275
990	17.4	0.2	19	1	CF291899	ACCESSION:CF291899	1063	17	0.2	25	1	BI094828	ACCESSION:BI094828
991	17.4	0.2	19	1	CF292072	ACCESSION:CF292072	1064	17	0.2	25	1	CF300714	ACCESSION:CF300714
992	17.4	0.2	19	1	CF292144	ACCESSION:CF292144	1065	17	0.2	25	1	CF315032	ACCESSION:CF315032
c 993	17.4	0.2	19	1	CF310688	ACCESSION:CF310688	c1066	17	0.2	25	1	AZ659095	ACCESSION:AZ659095
994	17.4	0.2	19	1	CF329136	ACCESSION:CF329136	c1067	17	0.2	25	1	TA12F02Q	ACCESSION:TA12F02Q
995	17.4	0.2	19	1	CF329136	ACCESSION:CF329136	c1068	17	0.2	26	1	AU265818	ACCESSION:AU265818
c 996	17.4	0.2	19	1	AZ450180	ACCESSION:AZ450180	c1069	17	0.2	26	1	AU268466	ACCESSION:AU268466
997	17.4	0.2	19	1	AZ513919	ACCESSION:AZ513919	c1070	17	0.2	26	1	AZ828616	ACCESSION:AZ828616
998	17.4	0.2	19	1	AZ645841	ACCESSION:AZ645841	c1071	17	0.2	28	1	AAB52828	ACCESSION:AAB52828
c 999	17.4	0.2	19	1	AZ650252	ACCESSION:AZ650252	1072	17	0.2	30	1	DR31A15T	ACCESSION:AL987581
1000	17.4	0.2	19	1	AZ654747	ACCESSION:AZ654747	c1073	17	0.2	31	1	AW245279	ACCESSION:AW245279
1001	17.4	0.2	20	1	CF297010	ACCESSION:CF297010	1074	17	0.2	34	1	BG5311309	ACCESSION:BG5311309
1002	17.4	0.2	20	1	CF333052	ACCESSION:CF333052	c1075	17	0.2	37	1	BX567522	ACCESSION:BX567522
1003	17.4	0.2	22	1	AZ307896	ACCESSION:AZ307896	1076	16.8	0.2	20	1	CF300961	ACCESSION:CF300961
1004	17.4	0.2	22	1	AZ845735	ACCESSION:AZ845735	1077	16.8	0.2	20	1	CF301101	ACCESSION:CF301101
c1005	17.4	0.2	23	1	AZ435597	ACCESSION:AZ435597	1078	16.8	0.2	20	1	CF336815	ACCESSION:CF336815
c1006	17.4	0.2	23	1	AZ862224	ACCESSION:AZ862224	1079	16.8	0.2	20	1	AZ343730	ACCESSION:AZ343730
1007	17.4	0.2	24	1	AZ399663	ACCESSION:AZ399663	c1080	16.8	0.2	20	1	AZ346143	ACCESSION:AZ346143
1008	17.4	0.2	25	1	CF319499	ACCESSION:CF319499	c1081	16.8	0.2	20	1	AZ633741	ACCESSION:AZ633741
1009	17.4	0.2	26	1	AU265518	ACCESSION:AU265518	1082	16.8	0.2	21	1	AW248782	ACCESSION:AW248782
c1010	17.4	0.2	26	1	AZ818035	ACCESSION:AZ818035	1083	16.8	0.2	21	1	CF319122	ACCESSION:CF319122
c1011	17.4	0.2	28	1	AZ824574	ACCESSION:AZ824574	c1084	16.8	0.2	21	1	CF319625	ACCESSION:CF319625
c1012	17.4	0.2	28	1	AZ836072	ACCESSION:AZ836072	1085	16.8	0.2	21	1	AZ468862	ACCESSION:AZ468862
1013	17.4	0.2	29	1	CF328476	ACCESSION:CF328476	1086	16.8	0.2	21	1	AZ597932	ACCESSION:AZ597932
c1014	17.4	0.2	30	1	CF299716	ACCESSION:CF299716	1087	16.8	0.2	21	1	AZ647578	ACCESSION:AZ647578
c1015	17.4	0.2	31	1	BQ591372	ACCESSION:BO591372	1088	16.8	0.2	22	1	AW246884	ACCESSION:AW246884
c1016	17.4	0.2	32	1	CF318239	ACCESSION:CF318239	1089	16.8	0.2	22	1	AZ345485	ACCESSION:AZ345485
1017	17.2	0.2	22	1	BQ591193	ACCESSION:BO591193	c1090	16.8	0.2	23	1	AZ662734	ACCESSION:AZ662734
1018	17.2	0.2	22	1	AZ442146	ACCESSION:AZ442146	1091	16.8	0.2	24	1	CF331867	ACCESSION:CF331867
1019	17.2	0.2	23	1	AW245956	ACCESSION:AW245956	c1092	16.8	0.2	24	1	CF331868	ACCESSION:CF331868
c1020	17.2	0.2	23	1	AZ382429	ACCESSION:AZ382429	1093	16.8	0.2	24	1	AZ782507	ACCESSION:AZ782507
c1021	17.2	0.2	23	1	AZ447220	ACCESSION:AZ447220	c1094	16.8	0.2	25	1	D19580	ACCESSION:D19580
c1022	17.2	0.2	24	1	AU257964	ACCESSION:AU257964	c1095	16.8	0.2	28	1	CF282351	ACCESSION:CF282351
c1023	17.2	0.2	24	1	AZ307138	ACCESSION:AZ307138	c1096	16.8	0.2	28	1	CF321885	ACCESSION:CF321885
1024	17.2	0.2	24	1	AZ514388	ACCESSION:AZ514388	c1097	16.8	0.2	28	1	CF330748	ACCESSION:CF330748
c1025	17.2	0.2	24	1	AZ814317	ACCESSION:AZ814317	1098	16.8	0.2	28	1	CF330938	ACCESSION:CF330938
1026	17.2	0.2	25	1	AW247153	ACCESSION:AW247153	c1099	16.8	0.2	28	1	CF3399637	ACCESSION:AZ399637
c1027	17.2	0.2	25	1	AZ348233	ACCESSION:AZ348233	1100	16.8	0.2	28	1	AZ401766	ACCESSION:AZ401766
1028	17.2	0.2	25	1	CG883604	ACCESSION:CG883604	c1101	16.8	0.2	28	1	AZ471744	ACCESSION:AZ471744
1029	17.2	0.2	30	1	BG865511	ACCESSION:BG865511	c1102	16.8	0.2	28	1	AZ493138	ACCESSION:AZ493138
1030	17.2	0.2	31	1	BG292912	ACCESSION:BG292912	c1103	16.8	0.2	28	1	AZ653365	ACCESSION:AZ653365
1031	17.2	0.2	32	1	CF302459	ACCESSION:CF302459	c1104	16.8	0.2	28	1	AZ785035	ACCESSION:AZ785035
c1032	17.2	0.2	32	1	AZ579652	ACCESSION:AZ579652	c1105	16.8	0.2	28	1	AZ824519	ACCESSION:AZ824519
c1033	17.2	0.2	32	1	DR1F7S	ACCESSION:AL735323	1106	16.8	0.2	28	1	AZ833425	ACCESSION:AZ833425
c1034	17.2	0.2	34	1	CF302250	ACCESSION:CF302250	c1107	16.8	0.2	28	1	AZ866569	ACCESSION:AZ866569
1035	17.2	0.2	35	1	BF338797	ACCESSION:BF338797	c1108	16.8	0.2	28	1	TA291A01Q	ACCESSION:AL486613
c1036	17	0.2	17	1	BQ590687	ACCESSION:BO590687	c1109	16.8	0.2	28	1	TA379D11P	ACCESSION:AL497637
1037	17	0.2	17	1	BQ591177	ACCESSION:BO591177	c1110	16.8	0.2	28	1	TA29A09P	ACCESSION:AL453073
1038	17	0.2	17	1	CF290854	ACCESSION:CF290854	c1111	16.8	0.2	28	1	CF279536	ACCESSION:CF279536
1039	17	0.2	17	1	CF295807	ACCESSION:CF295807	1112	16.8	0.2	29	1	CF299920	ACCESSION:CF299920
1040	17	0.2	17	1	CF298589	ACCESSION:CF298589	1113	16.8	0.2	29	1	CF312601	ACCESSION:CF312601
1041	17	0.2	17	1	CF299639	ACCESSION:CF299639	1114	16.8	0.2	29	1	AZ389566	ACCESSION:AZ389566
1042	17	0.2	17	1	CF310219	ACCESSION:CF310219	c1115	16.8	0.2	29	1	AZ414283	ACCESSION:AZ414283
1043	17	0.2	17	1	CF334566	ACCESSION:CF334566	c1116	16.8	0.2	29	1	AZ451930	ACCESSION:AZ451930
c1044	17	0.2	18	1	AL048754	ACCESSION:AL048754	c1117	16.8	0.2	29	1	AZ468402	ACCESSION:AZ468402
1045	17	0.2	18	1	CF301057	ACCESSION:CF301057	c1118	16.8	0.2	29	1	AZ486793	ACCESSION:AZ486793
1046	17	0.2	18	1	CF301151	ACCESSION:CF301151	c1119	16.8	0.2	29	1	AZ6661709	ACCESSION:AZ6661709
1047	17	0.2	19	1	CF327587	ACCESSION:CF327587	1120	16.8	0.2	29	1	AZ784208	ACCESSION:AZ784208
c1048	17	0.2	19	1	AZ345795	ACCESSION:AZ345795	1121	16.8	0.2	29	1	AZ806470	ACCESSION:AZ806470
1049	17	0.2	19	1	AZ650575	ACCESSION:AZ650575	1122	16.8	0.2	29	1	AZ812242	ACCESSION:AZ812242
c1050	17	0.2	19	1	AZ853220	ACCESSION:AZ853220	1123	16.8	0.2	29	1	AZ868731	ACCESSION:AZ868731
1051	17	0.2	20	1	CF298018	ACCESSION:CF298018	c1124	16.8	0.2	29	1	TA334G09Q	ACCESSION:AL491938
1052	17	0.2	20	1	CF319428	ACCESSION:CF319428	c1125	16.8	0.2	30	1	AZ458127	ACCESSION:AZ458127
c1053	17	0.2	20	1	AZ818055	ACCESSION:AZ818055	1126	16.8	0.2	30	1	BG666435	ACCESSION:BG666435
c1054	17	0.2	21	1	AL048772	ACCESSION:AL048772	c1127	16.8	0.2	30	1	CF280699	ACCESSION:CF280699
1055	17	0.2	21	1	AZ610868	ACCESSION:AZ610868	1128	16.8	0.2	30	1	CF292086	ACCESSION:CF292086

c1129	16.8	0.2	30	1	CF299555	ACCESSION:CF299555
c1130	16.8	0.2	30	1	CF312417	ACCESSION:CF312417
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c1274	16	0.2	27	1	RS9382	ACCESSION:RS9382



[illegible]





Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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 High quality sequence stop: 50.

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 DEFINITION 2M0167013R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0167013 R, genomic survey sequence.

ACCESSION  
 VERSION AZ861400.1 GI:13057682  
 KEYWORDS GSS.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 35)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
 Unpublished (2000)

COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center

University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606

Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
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LOCUS 39 bp DNA linear GSS 27-APR-2001

DEFINITION 2M0269N24F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0269N24 F, genomic survey sequence.

ACCESSION  
 VERSION AZ987023  
 KEYWORDS GSS.

SOURCE  
 Mus musculus (house mouse)

ORGANISM  
 Mus musculus

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 1 (bases 1 to 39)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL  
 Unpublished (2000)

COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center

University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177











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CF328492
LOCUS      CF328492      34 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--03-G22.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-G22, mRNA sequence.
ACCESSION CF328492
VERSION   CF328492.1 GI:33805230
KEYWORDS  EST.
SOURCE    Oryza sativa
ORGANISM  Oryza sativa
REFERENCE 1 (bases 1 to 34)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL   Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongui University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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ACCESSION AZ485624
VERSION   AZ485624.1 GI:10651606
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SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 26)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weise,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
JOURNAL   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA

CF328492
LOCUS      CF328492      34 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION NACL--03-G22.b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-G22, mRNA sequence.
ACCESSION CF328492
VERSION   CF328492.1 GI:33805230
KEYWORDS  EST.
SOURCE    Oryza sativa
ORGANISM  Oryza sativa
REFERENCE 1 (bases 1 to 34)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL   Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongui University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

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Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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VERSION   AZ485624.1 GI:10651606
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE 1 (bases 1 to 26)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weise,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Unpublished (2000)
JOURNAL   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA

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Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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   /mol_type="genomic DNA"
   /strain="C57BL/6J"
   /db_xref="taxon:10090"
   /clone="UUGCLM0313H1"
   /sex="Male"
   /lab_hosts="E. Coli strain XL10-Gold, Tl-resistant, F-"
   /clone_lib="Mouse 10kb plasmid UUGCLM library"
   /note="Vector: PWD42nv; Purified genomic DNA from M.
   musculus C57BL/6J (male) was obtained from the Jackson
   Laboratory Mouse DNA Resource
   (http://www.jax.org/resources/documents/dnares/). The DNA
   was hydrodynamically sheared by repeated passage through a
   0.005 inch orifice at constant velocity. The sheared DNA
   was blunt end-repaired with T4 DNA polymerase and T4
   polynucleotide kinase. Adaptor oligonucleotides were
   ligated to the blunt ends in high molar excess. The
   adaptor DNA was purified and size-selected for a 9.5 to
   10.5 kb range using preparative agarose gel
   electrophoresis. Vector DNA was prepared from a derivative
   of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
   inducible derivative of plasmid R1. The vector was ligated
   with adaptors complementary to the insert adaptors and
   purified. The sheared, adaptor mouse DNA was annealed to
   adaptor vector DNA, and transformed into
   chemically-competent E. coli XL10-Gold (Stratagene) cells
   and selected for ampicillin resistance."

Query Match      0.3%; Score 23.4; DB 1; Length 26;
Best Local Similarity 96.0%; Pred. No. 85;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4458 ATGCACCTTTTTCCTTTTTCCTTTTTCCTTTT 4482
      |||||
Db    25 ATGCATTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTT 1

RESULT 17
T52836
LOCUS      T52836      28 bp      mRNA      linear      EST 06-FEB-1995
DEFINITION Ya81b09.g1 Stratagene ovary (#937217) Homo sapiens cDNA clone
IMAGE:68057 3', similar to similar to gb:X53463 GLUTATHIONE
PEROXIDASE-GASTROINTESTINAL (HUMAN), mRNA sequence.
ACCESSION T52836
VERSION   T52836.1 GI:654696
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 28)
AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
          Chisoe,S., Dietrich,N., DuBueque,T., Favello,A., Gieh,W.,
          Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
          Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
          Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
          Trevaaskis,E., Underwood,K., Wohlmann,P., Waterston,R., Wilson,R.
          and Marra,M.
TITLE     Generation and analysis of 280,000 human expressed sequence tags
JOURNAL   Genome Res. 6 (9), 807-828 (1996)
MEDLINE   97044478
PUBMED    8889549
COMMENT   Contact: Wilson RK

```

Class: plasmid ends  
High quality sequence stop: 28.

## FEATURES

## FEATURES









QY 4463 CTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488  
 DB 1 CTTTCTTTTCTTTTCTTTTCTTTTCTTTT 26

RESULT 31  
 BQ590537  
 LOCUS  
 DEFINITION BQ590537 29 bp mRNA linear EST 06-DEC-2002  
 CDNA clone 024-019-C03-T7 MP12-ADIS-024-storage root Beta vulgaris  
 ACCESSION BQ590537  
 VERSION BQ590537  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 29)  
 Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 12472698  
 Contact: Weisshaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weisshaar@mpiz-koeln.mpg.de  
 Insert Length: 29 Std Error: 0.00  
 Plate: 19 row: C column: 03  
 Seq primer: T7; GTAATACGACTCACTATAGGCG.  
 Location/Qualifiers  
 1..29  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:189579"  
 /db\_xref="taxon:161934"  
 /clone="024-019-C03"  
 /tissue\_type="storage root"  
 /lab\_hosts="EMDH10B"  
 /clone\_libs="MP12-ADIS-024-storage root"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-SalI-CCACCGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 22.8; DB 1; Length 29;  
 Best Local Similarity 92.3%; Pred. No. 1.4e+02;  
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTTTCTTTG 4489  
 DB 3 TTTTCTTTTCTTTTCTTTTCTTTTCTTTG 28

RESULT 32  
 T67079/c  
 LOCUS  
 DEFINITION ya52f07.r3 Soares fetal liver spleen INFLS Homo sapiens cDNA clone

IMAGE:66565 5' similar to gb:X02492 INTERFERON-INDUCED PROTEIN 6-16  
 PRECURSOR (HUMAN); mRNA sequence.

T67079  
 T67079.1 GI:676519  
 EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 29)  
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,  
 Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,  
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,  
 Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and  
 Wilson,R.  
 The WashU-Merck EST Project  
 Unpublished (1995)  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 High quality sequence starts: 1  
 High quality sequence stops: 1  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Seq primer: T7  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..29  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:66565"  
 /sex="male"  
 /dev\_stage="20 week-post conception fetus"  
 /lab\_hosts="DH10B (ampicillin resistant)"  
 /clone\_libs="Soares fetal liver spleen INFLS"  
 /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)  
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;  
 1st strand cDNA was primed with a Pac I - oligo(dT) primer  
 [5' AACTGGAAGAATTAATAAGATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Pac I and cloned into the Pac I  
 and Eco RI sites of the modified pT7T3 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.3%; Score 22.8; DB 1; Length 29;  
 Best Local Similarity 88.9%; Pred. No. 1.4e+02;  
 Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4466 TTTTCTTTTCTTTTCTTTTCTTTTCTTTGAGA 4492  
 DB 29 TTTTCTTTTCTTTTCTTTTCTTTTCTTTGAGA 3

RESULT 33  
 BG865511/c  
 LOCUS  
 DEFINITION BG865511 30 bp mRNA linear EST 29-MAY-2001  
 602783643F1 NCI\_CGAP\_SG2 Mus musculus cDNA clone IMAGE:4909811 5',  
 mRNA sequence.  
 ACCESSION BG865511  
 VERSION BG865511.1 GI:14216051  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 1 (bases 1 to 30)

```

AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgabs-r@mail.nih.gov
              CDNA Library Preparation: Life Technologies, Inc.
              CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM10809 row: e column: 12
              High quality sequence stop: 30.

FEATURES     source
              1. .30
                /organism="Mus musculus"
                /mol_type="mRNA"
                /strain="FVB/N"
                /db_xref="taxon:10090"
                /clone="IMAGE:4909811"
                /lab_host="DH10B (T1 phage-resistant)"
                /clone_lib="NCI CGAP SG2"
                /notes="Organ: salivary gland; Vector: pCMV-SPORT6; Site 1:
                NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo
                dt. Average insert size 1.3 kb. Constructed by Life
                Technologies. Note: this is a NCI CGAP Library."

              Query Match      0.3%; Score 22.8; DB 1; Length 30;
              Best Local Similarity 92.3%; Pred. No. 1.5e+02;
              Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
DB 30 CTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 5

RESULT 34
A2962183/c
LOCUS      A2962183
DEFINITION 2M0230124R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0230124 R, genomic survey sequence.
ACCESSION  A2962183
VERSION     A2962183.1 GI:13833410
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 30)
REFERENCE   1
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0230 row: I column: 24
            Seq primer: CACACGAAACACCTATGACC
            Class: plasmid ends
            High quality sequence stop: 30.
            Location/Qualifiers
              1. .30
                /organism="Mus musculus"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0230124"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (GI4732114|9b|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

              Query Match      0.3%; Score 22.8; DB 1; Length 30;
              Best Local Similarity 92.3%; Pred. No. 1.5e+02;
              Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
DB 27 CTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 2

RESULT 35
BG292912/c
LOCUS      BG292912
DEFINITION 602389549F1 NIH_MGC_94 Mus musculus CDNA clone IMAGE:4501164 5',
mRNA sequence.
ACCESSION  BG292912
VERSION     BG292912.1 GI:13052227
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 31)
REFERENCE   1
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: The Cepko Laboratory
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10368 row: b column: 13
            High quality sequence stop: 31.
            Location/Qualifiers
              1. .31
                /organism="Mus musculus"
                /mol_type="mRNA"
                /db_xref="taxon:10090"
                /clone="IMAGE:4501164"
                /tissue_type="retina"
                /lab_host="DH10B (phage-resistant)"
                /clone_lib="NIH MGC 94"
                /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;

```

Site 2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."

Query Match 0.3%; Score 22.8; DB 1; Length 31;  
Best Local Similarity 92.3%; Pred. No. 1.7e+02;  
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 4463 CTTTTTTTTTTTTTTTTTTTGTCT 4488  
Db 31 CTTTTTTTTTTTTTTTTTTT 6

RESULT 36  
AL587570  
LOCUS  
DEFINITION AL587570 BP Chicken Brain Library Gallus gallus cDNA clone  
ROS059B09, mRNA sequence.

ACCESSION  
VERSION AL587570.1 GI:13192604  
KEYWORDS  
SOURCE EST.

ORGANISM  
Gallus gallus (chicken)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BP Chicken Brain Library  
Unpublished (2001)  
Contact: Frazer Murray  
Dept. Genomics and Bioinformatics

Roslin Institute  
Roslin, Midlothian, EH25 9PS, UK  
Tel: +44 (0)131 527 4200  
Fax: +44 (0)131 440 0434

Email: frazer.murray@bbsrc.ac.uk  
GCGCCGCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clonetechn

(\*6854-  
Seq primer: M13F.

FEATURES  
source  
Location/Qualifiers

1..32  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="ROS059B09"  
/tissue\_type="Brain"  
/dev\_stage="Unknown"  
/lab\_host="DH10B"  
/clone\_lib="BP Chicken Brain Library"

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned  
unidirectionally. Primer: oligo dt. 5' adaptor sequence:  
5' TCGACCTGAG 3'; 3' adaptor sequence: 5'  
CGCCGCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from  
Clonetechn (\*6854-1)"

Query Match 0.3%; Score 22.8; DB 1; Length 32;  
Best Local Similarity 92.3%; Pred. No. 1.8e+02;  
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4465 TTTTTTTTTTTTTTTTTTTTGTCTGA 4490  
Db 3 TTTTTTTTTTTTTTTTTTTTCTTA 28

RESULT 37

CF302459/c

LOCUS

DEFINITION CF302459 7LEAF--08-A01.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--08-A01, mRNA sequence.

ACCESSION  
VERSION CF302459

CF302459.1 GI:33674220

KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS

1 (bases 1 to 32)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University

Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

FEATURES  
source

1..32  
/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clones="7LEAF--08-A01"

/tissue\_type="leaf"

/dev\_stage="7 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"

/note="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 22.8; DB 1; Length 32;  
Best Local Similarity 92.3%; Pred. No. 1.8e+02;  
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTTGTCTTG 4489  
Db 28 TTTTTTTTTTTTTTTTTTTT 3

RESULT 38

AZ579652

LOCUS

DEFINITION

1M0367C12R Mouse 10kb plasmid UGCCIM library Mus musculus genomic

clone UGCCIM0367C12 R, genomic survey sequence.

ACCESSION  
VERSION

AZ579652.1 GI:11694081

KEYWORDS  
SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 32)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rally, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0367 row: C column: 12  
Seq primer: CACACAGGAACACGATATGACC

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Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1. .32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0367C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 22.8; DB 1; Length 32;
Best Local Similarity 92.3%; Pred. No. 1.8e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTTTTTGCTT 4488
|||||
Db 2 CTTTTTTTTTTTTTTTTTTT 27

RESULT 39
LOCUS DRI1F7S 32 bp DNA linear GSS 27-NOV-2002
DEFINITION Danio rerio genomic clone DKEY-1F7, genomic survey sequence.
ACCESSION AL735323
VERSION AL735323.1 GI:21343938
KEYWORDS GSS.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 32)
Humphray,S.J., Huckle,E. and Hunt,S.E.
Direct Submission
Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humquerry@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 1F7. 1F7 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene.
Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
Location/Qualifiers
1. .32
/organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-1F7"
/tissue_type="Testis"
/notes="vector pindigoBAC-536"

Query Match 0.3%; Score 22.8; DB 1; Length 32;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1. .33
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0552E03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 22.8; DB 1; Length 33;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTGCTTG 4489
|||||
Db 6 TTTTTTTTTTTTTTTTTTTT 31

RESULT 40
LOCUS AZ759642 33 bp DNA linear GSS 16-FEB-2001
DEFINITION clone UUGC1M0552E03 R, genomic survey sequence.
ACCESSION AZ759642
VERSION AZ759642.1 GI:12866639
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 33)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0552 row: E column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1. .33
/organism="Mus musculus"
/mol_type="genomic DNA"
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/clone="UUGC1M0552E03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 22.8; DB 1; Length 33;
Best Local Similarity 92.3%; Pred. No. 1.9e+02;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTCTTTTCTTTTCTTTCTTTCTTT 4488  
 |||||  
 Db 3 CTTTCTTTTCTTTTCTTTCTTTCTTT 28

AV674152 34 bp mRNA linear EST 05-OCT-2000  
 AV674152 Nori Satoh unpublished cDNA library Ciona intestinalis  
 CNA clone citb14i22 5', mRNA sequence.  
 ACCESSION AV674152  
 VERSION AV674152.1 GI:10112151  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Clonidae; Ciona.  
 REFERENCE 1 (bases 1 to 34)  
 AUTHORS Satoh, N., Satou, Y., Kohara, Y. and Shin, I., T.  
 TITLE Expressed genes in Ciona intestinalis  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Nori Satoh  
 Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4081  
 Fax: 81-75-705-1113  
 Email: satohascidian.zool.kyoto-u.ac.jp.

FEATURES  
 source  
 1..34  
 /organism="Ciona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="citb14i22"  
 /tissue\_type="whole animal"  
 /dev\_stages="tailbud"  
 /clone\_lib="Nori Satoh unpublished cDNA library"

Query Match 0.3%; Score 22.8; DB 1; Length 34;  
 Best Local Similarity 92.3%; Pred. No. 2.1e+02;  
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTCTTTTCTTTTCTTTCTTTCTTT 4488  
 |||||  
 Db 2 CTTTCTTTTCTTTTCTTTCTTTCTTT 27

AV674152 34 bp mRNA linear EST 14-AUG-2003  
 AV674152 Nori Satoh unpublished cDNA library (14ROOT) Oryza  
 sativa cDNA clone 14ROOT--02-M02, mRNA sequence.  
 ACCESSION CF292071  
 VERSION CF292071.1 GI:33661104  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 34)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Query Match 0.3%; Score 22.8; DB 1; Length 34;  
 Best Local Similarity 92.3%; Pred. No. 2.1e+02;  
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4463 CTTTCTTTTCTTTTCTTTCTTTCTTT 4488  
 |||||  
 Db 2 CTTTCTTTTCTTTTCTTTCTTTCTTT 27

CF292071 34 bp mRNA linear EST 14-AUG-2003  
 CF292071 14ROOT--02-M02.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
 sativa cDNA clone 14ROOT--02-M02, mRNA sequence.  
 ACCESSION CF292071  
 VERSION CF292071.1 GI:33661104  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 34)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355

Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..34  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="14ROOT--02-M02"  
 /tissue\_type="root"  
 /dev\_stages="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 22.8; DB 1; Length 34;  
 Best Local Similarity 79.4%; Pred. No. 2.1e+02;  
 Matches 27; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4469 TTTTCTTTTCTTTTCTTTCTTTCTTTCTTT 4502  
 |||||  
 Db 1 TTTTCTTTTCTTTTCTTTCTTTCTTTCTTT 34

CF302250 34 bp mRNA linear EST 15-AUG-2003  
 CF302250 7LEAF--07-J10.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--07-J10, mRNA sequence.  
 ACCESSION CF302250  
 VERSION CF302250.1 GI:33674011  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 34)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
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 1..34  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="7LEAF--07-J10"  
 /tissue\_type="leaf"  
 /dev\_stages="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 22.8; DB 1; Length 34;  
 Best Local Similarity 92.3%; Pred. No. 2.1e+02;  
 Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTCTTTCTTTCTTT 4489  
 |||||  
 Db 8 TTTTCTTTTCTTTTCTTTCTTTCTTTCTTT 33

REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 35)
TITLE	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999)
	Contact: Robert Strausberg, Ph.D.
	Email: <a href="mailto:cgaps-f@mail.nih.gov">cgaps-f@mail.nih.gov</a>
	Tissue Procurement: David N. Louis, M.D.
	cDNA Library Preparation: Life Technologies, Inc.
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
	DNA Sequencing by: Incyte Genomics, Inc.

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0091 row: A column: 19  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 29.  
Location/Qualifiers  
1. .29  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="YUGC2M0091A19"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGCIM library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson



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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:56461"
/sex="male"
/dev_stages="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver spleen 1NFS"
/note="Organ: Liver and Spleen; Vector: pTV73D (Pharmacina)
/note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not
I; Site 2: Hind III; 1st strand cDNA was primed with a Not
I - oligo(dT) primer [5'
AATGTGAAGAATTGGCGCGCCAGGAATTTTTTTTTTTTTTTT 3'] ;
double-stranded cDNA was ligated to Hind III adaptors
(Pharmacina), digested with Not I and directionally cloned
into the Not I and Hind III sites of the Lafmid BA vector.
Library went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Ronaldo."

```



Query Match 0.3%; Score 22.4; DB 1; Length 32;

RESULT 54	AZ307192/c	AZ307192	34 bp	DNA	linear	GSS 29-SEP-2000
LOCUS	AZ307192/c	1M000807R	Mouse 10kb	plasmid	UUGCIM library	Mus musculus genomic
DEFINITION	AZ307192	clone UUGCIM000807 R,	genomic survey	sequence.		
ACCESSION	AZ307192					
VERSION	AZ307192.1	GI:10345947				

**KEYWORDS**  
Mus musculus (house mouse)

**SOURCE ORGANISM**  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 34)

**REFERENCE AUTHORS**  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Iglam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weise,R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

**JOURNAL COMMENT**  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0008 row: B column: 07  
Seq primer: CACACGAGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 34.

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1..34  
    /organism="Mus musculus"  
    /mol\_type="genomic DNA"  
    /strain="C57BL/6J"  
    /db\_xref="taxon:10090"  
    /clone="UUGC1M0008B07"  
    /sex="Male"  
    /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
    /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
    /note="vector: PWD42nv; Purified genomic DNA from M.  
        musculus C57BL/6J (male) was obtained from the Jackson  
        Laboratory Mouse DNA Resource  
        (http://www.jax.org/resources/documents/dnares/). The DNA  
        was hydrodynamically sheared by repeated passage through a  
        0.005 inch orifice at constant velocity. The sheared DNA  
        was blunt end-repaired with T4 DNA polymerase and T4  
        polynucleotide kinase. Adaptor oligonucleotides were  
        ligated to the blunt ends in high molar excess. The  
        adaptored DNA was purified and size-selected for a 9.5 to  
        10.5 kb range using preparative agarose gel  
        electrophoresis. Vector DNA was prepared from a derivative  
        of pW42 [gi|4732114|gb|AF129072.1], a copy-number  
        inducible derivative of plasmid R1. The vector was ligated  
        with adaptors complementary to the insert adaptors and  
        purified. The sheared, adaptored mouse DNA was annealed to  
        adaptored vector DNA, and transformed into  
        chemically-competent E. coli XL10-Gold (Stratagene) cells  
        and selected for ampicillin resistance."

Query Match	0.3%	Score 22.4	DB 1	Length 34;
Best Local Similarity	95.8%	Pred.No. 2.4e+02;		
Matches 23;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

**QY** 4465 TTTTTCCTTTTTTTTTTTTGCTT 4488

**DB** 34 TTTTTCCTTTTTTTTTTTTGCTT 11

**RESULT 55**  
CF337400/c

**LOCUS**  
CF337400 28 bp mRNA linear EST 18-AUG-2003

**DEFINITION**  
JMT--07-N04\_g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
library (JMT) Oryza sativa cDNA clone JMT--07-N04, mRNA sequence.

**ACCESSION**  
VERSION  
CF337400.1 GI:33823200

**KEYWORDS**  
EST.

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1. .31
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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FEATURES
source
Location/Qualifiers
1..32
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"

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/clone="UUGC1M0162P23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 22.2; DB 1; Length 32;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4462 ACTTTTGTGCTT 4488
Db 30 AATTTTTTTTTTTTTTTTTTTTTT 4

RESULT 59
AZ400441/c
LOCUS
DEFINITION
M0166C14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0166C14 R, genomic survey sequence.
ACCESSION
AZ400441
VERSION
AZ400441.1 GI:10515515
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0166 row: C column: 14
Seq primer: CACACGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 32.
Location/Qualifiers
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0166C14"

FEATURES
source
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pPW42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 22.2; DB 1; Length 32;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4462 ACTTTTGTGCTT 4488
Db 32 AATTTTTTTTTTTTTTTTTTTTTT 6

RESULT 60
AL587609
LOCUS
DEFINITION
AL587609 BP Chicken Brain Library Gallus gallus cDNA clone
ROS059G05, mRNA sequence.
ACCESSION
AL587609
VERSION
AL587609.1 GI:13192643
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 33)
Murray,F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCTTTTGTGCTT 3' Poly A RNA purchased from Clontech
(*6854-
Seq primer: M13F.
Location/Qualifiers
1..33
/organism="Gallus gallus"
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/clone="ROS059G05"
/tissue_type="Brain"
/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5'
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCTTTTGTGCTT 3' Poly A RNA purchased from
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RESULT 62	AL587876	34 bp	mRNA	linear	EST 02-MAR-2001
LOCUS	AL587876				
DEFINITION	AL587876 BP Chicken Brain Library Gallus gallus cDNA clone ROS064F10, mRNA sequence.				
ACCESSION	AL587876				

BU431802 34 bp mRNA linear EST 09-SEP-2002  
601654630R1 NIH\_MGC\_57 Homo sapiens cDNA clone IMAGE:3839742 3',  
mRNA sequence.  
BU431802  
BU431802.1 GI:22770284  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 34)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabos-remail.nih.gov](mailto:cgabos-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: CLONETECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCMS28 row: k column: 07  
High quality sequence stop: 34.

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FEATURES
source
1. 34
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3839742"
/tissue_type="glioblastoma"
/lab_host="DH10B (Ti phage-resistant)"
/clone_lib="NIH_MGC_57"
/notes="Organ: brain; Vector: pDNR-LIB (Clontech); Site_1:
sfli (ggccgctcgcc); Site_2: sfli (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCCGAGCGCGGCACATG-CT(30)BN-3'
(where B = A, C, G, or T). Average
insert size 1.55 kb (range 0.9-4.0 kb). 12/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

Query Match 0.3%; Score 22.2; DB 1; Length 34;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 24; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTTGCTCTGA 4490
| | | | | | | | | | | | | | | | | | | |
Db 3 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTGA 29

RESULT 64
BX559898
LOCUS
DEFINITION BX559898 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse46d05_pic, mRNA sequence.
ACCESSION BX559898
VERSION
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
1 (bases 1 to 23)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
2881942
PUBMED
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
1. 23
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse46d05_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected

gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 22; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTTTGT 4485
| | | | | | | | | | | | | | | | | | | |
Db 1 TTTTCTTTTCTTTTCTTTTCTTTTGT 22

RESULT 65
CF299716
LOCUS
DEFINITION 7LEAF--03-N11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-N11, mRNA sequence.
ACCESSION CF299716
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 30)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, Y.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. 30
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--03-N11"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 22; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTTTGT 4485
| | | | | | | | | | | | | | | | | | | |
Db 1 TTTTCTTTTCTTTTCTTTTCTTTTGT 22

RESULT 66
AZ869514/c
LOCUS
DEFINITION 2M0181107R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0181107 R, genomic survey sequence.
ACCESSION AZ869514
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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T.brucei"

Query Match      0.3%; Score 22; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTTGTCTT 4488
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTTGTGTTT 33

RESULT 69
BX553142
LOCUS BX553142 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION BX553142 Glossina morsitans cDNA clone Tse127f01_pic, mRNA sequence.
ACCESSION BX553142
VERSION BX553142.1 GI:33377335
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 33)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinnton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
1. .33
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse127f01_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.3%; Score 22; DB 1; Length 33;
Best Local Similarity 83.3%; Pred. No. 2.7e+02;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTTGTCTT 4488
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTTGTGTTT 33

RESULT 71
CF291048
LOCUS CF291048 25 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ROOT--01-F05.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-F05, mRNA sequence.
ACCESSION CF291048
VERSION CF291048.1 GI:33660081
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 25)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193

Query Match      0.3%; Score 22; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTTGT 4485
Db 12 TTTTTTTTTTTTTTTTTTTTGT 33

RESULT 70
BX566898
LOCUS BX566898 33 bp mRNA linear EST 14-OCT-2003
DEFINITION BX566898 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse84h03_pic, mRNA sequence.
ACCESSION BX566898

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[illegible]

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
REFERENCE
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
        Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
        Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
        Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
           University of Utah Genome Center
           University of Utah
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000 Std Error: 0.00
           Plate: 0078 row: I column: 24
           Seq primer: CACACAGGAACAGCTATGACC
           Class: plasmid ends
           High quality sequence stop: 25.
FEATURES   Location/Qualifiers
source     1. .25
           /organism="Mus musculus"
           /mol_type="genomic DNA"
           /strain="C57BL/6J"
           /db_xref="taxon:10090"
           /clone="UUGC1M0078124"
           /sex="Male"
           /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
           /clone_lib="Mouse 10kb plasmid UUGC1M library"
           /notes="Vector: PWD42nv; Purified genomic DNA from M.
           musculus C57BL/6J (male) was obtained from the Jackson
           Laboratory Mouse DNA Resource
           (http://www.jax.org/resources/documents/dnares/). The DNA
           was hydrodynamically sheared by repeated passage through a
           0.005 inch orifice at constant velocity. The sheared DNA
           was blunt end-repaired with T4 DNA polymerase and T4
           polynucleotide kinase. Adaptor oligonucleotides were
           ligated to the blunt ends in high molar excess. The
           adaptor DNA was purified and size-selected for a 9.5 to
           10.5 kb range using preparative agarose gel
           electrophoresis. Vector DNA was prepared from a derivative
           of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
           inducible derivative of plasmid R1. The vector was ligated
           with adaptors complementary to the insert adaptors and
           purified. The sheared, adaptor mouse DNA was annealed to
           adaptor vector DNA, and transformed into
           chemically-competent E. coli XL10-Gold (Stratagene) cells
           and selected for ampicillin resistance."
Query Match      0.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
      |||||
Db 25 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 81
AZ350777
LOCUS      AZ350777
DEFINITION 1M0088A04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0088A04 R, genomic survey sequence.
ACCESSION  AZ350777
VERSION     AZ350777.1
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
REFERENCE
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
        Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
        Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
        Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
           plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
           University of Utah Genome Center
           University of Utah
           Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
           84112, USA
           Tel: 801 585 5606
           Fax: 801 585 7177
           Email: ddunn@genetics.utah.edu
           Insert Length: 10000 Std Error: 0.00
           Plate: 0078 row: I column: 24
           Seq primer: CACACAGGAACAGCTATGACC
           Class: plasmid ends
           High quality sequence stop: 25.
FEATURES   Location/Qualifiers
source     1. .25
           /organism="Mus musculus"
           /mol_type="genomic DNA"
           /strain="C57BL/6J"
           /db_xref="taxon:10090"
           /clone="UUGC1M0088A04"
           /sex="Male"
           /lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
           /clone_lib="Mouse 10kb plasmid UUGC1M library"
           /notes="Vector: PWD42nv; Purified genomic DNA from M.
           musculus C57BL/6J (male) was obtained from the Jackson
           Laboratory Mouse DNA Resource
           (http://www.jax.org/resources/documents/dnares/). The DNA
           was hydrodynamically sheared by repeated passage through a
           0.005 inch orifice at constant velocity. The sheared DNA
           was blunt end-repaired with T4 DNA polymerase and T4
           polynucleotide kinase. Adaptor oligonucleotides were
           ligated to the blunt ends in high molar excess. The
           adaptor DNA was purified and size-selected for a 9.5 to
           10.5 kb range using preparative agarose gel
           electrophoresis. Vector DNA was prepared from a derivative
           of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
           inducible derivative of plasmid R1. The vector was ligated
           with adaptors complementary to the insert adaptors and
           purified. The sheared, adaptor mouse DNA was annealed to
           adaptor vector DNA, and transformed into
           chemically-competent E. coli XL10-Gold (Stratagene) cells
           and selected for ampicillin resistance."
Query Match      0.3%; Score 21.8; DB 1; Length 25;
Best Local Similarity 92.0%; Pred. No. 1.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
      |||||
Db 25 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 82
AZ389458/c
LOCUS      AZ389458/c
DEFINITION 1M0150B06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0150B06 F, genomic survey sequence.
ACCESSION  AZ389458
VERSION     AZ389458.1
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```









project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: neleayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source  
1. .25  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="324e10"

Query Match 0.3%; Score 21.8; DB 1; Length 25;  
Best Local Similarity 92.0%; Pred. No. 1.5e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTGTCTTTTGTCTT 4488  
|||||  
Db 1 TTTTGTCTTTTGTCTT 25

## RESULT 89

AL587774  
LOCUS  
DEFINITION  
AL587774 BP Chicken Brain Library Gallus gallus cDNA clone  
ROS063A11, mRNA sequence.

ACCESSION  
AL587774  
VERSION  
AL587774.1 GI:13192808  
KEYWORDS  
EST.

SOURCE  
Gallus gallus (chicken)

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

REFERENCE  
1 (bases 1 to 26)

AUTHORS  
Murray, F.

TITLE  
BP Chicken Brain Library

JOURNAL  
Unpublished (2001)

COMMENT  
Contact: Frazer Murray,  
Dept. Genomics and Bioinformatics  
Roslin Institute

Roslin, Midlothian, EH25 9PS, UK

Tel: +44 (0)131 527 4200

Fax: +44 (0)131 440 0434

Email: frazer.murray@bbsrc.ac.uk  
GCGGCGCTTTTGTCTT 3' Poly A RNA purchased from Clontech

(\*6854-

## FEATURES

source  
1. .26  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="ROS063A11"  
/tissue\_type="Brain"  
/dev\_stage="Unknown"  
/lab\_host="DH10B"

/clone\_lib="BP Chicken Brain Library"  
/note=vector: pSPORt1; Site 1: Not1; Site 2: Sal1; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5' GCGGCGCTTTTGTCTT 3' Poly A RNA purchased from

## Clontech (\*6854-1)"

Query Match 0.3%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 1.6e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTGTCTTTTGTCTT 4488  
|||||  
Db 2 TTTTGTCTTTTGTCTT 26

## RESULT 90

AW327613  
LOCUS  
DEFINITION  
AW327613 26 bp mRNA linear EST 28-JAN-2000  
cqlb09.y1 NIH\_MGC\_2 Homo sapiens cDNA clone IMAGE:2846536 3', mRNA sequence.

ACCESSION  
AW327613  
VERSION  
AW327613.1 GI:6798108

KEYWORDS  
EST.

SOURCE  
Homo sapiens (human)

ORGANISM  
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1 (bases 1 to 26)

AUTHORS  
NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE  
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL  
Unpublished (1999)

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Edge Biosystems

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: NIH Intramural Sequencing Center (NISC)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Plate: LLCM0028 row: C column: 17

Seq primer: M13RPI reverse primer (ABI).

## FEATURES

source  
1. .26  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2846536"  
/tissue\_type="T cell leukemia"  
/cell\_line="MGC2"  
/clone\_lib="NIH MGC 2"  
/note="Organ: Blood; Vector: pOTB7a; Library prepared by Edge Biosystems."

Query Match 0.3%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 1.6e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTGTCTTTTGTCTT 4488  
|||||  
Db 1 TTTTGTCTTTTGTCTT 25

## RESULT 91

CF278359  
LOCUS  
DEFINITION  
CF278359 26 bp mRNA linear EST 14-AUG-2003  
14ETL--04-D22.g1 Rice etiolated leaf plasmid cDNA library (14ETL)

ACCESSION  
CF278359  
VERSION  
CF278359.1 GI:33655745

KEYWORDS  
EST.

SOURCE  
Oryza sativa

ORGANISM  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE  
1 (bases 1 to 26)















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FEATURES
source
high quality sequence map: 26.
Location/Qualifiers
1. .26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0474H08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

FEATURES
source
1. .26
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0525H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed into adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match 0.3%; Score 21.8; DB 1; Length 26;  
Best Local Similarity 92.0%; Pred. No. 1.6e+02;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTCCTT 4488  
 Db 1 TTTT...TTTTCCTT 25

RESULT 110  
 TA324D07P/C 26 bp DNA linear GSS 13-DEC-2000  
 LOCUS T. brucei sheared genomic DNA clone 324D07, forward sequence,  
 DEFINITION genomic survey sequence.  
 ACCESSION AL493390 GI:11867755  
 VERSION AL493390.1  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.  
 1 (bases 1 to 26)  
 Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
 Melville, S.E., Rajadream, M.A. and Barrell, B.G.  
 Direct Submission  
 Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
 nh@sanger.ac.uk  
 Constructed at the Institute for Genomic Research (TIGR),  
 Rockville, MD. Genomic DNA isolated from a cloned population of  
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
 to give a tight size distribution (4 kb). The v + i method used for the library construction is  
 described in detail in Smith, H. and Venter, J.C. (Making small  
 insert libraries for whole genome shotgun sequencing projects. In  
 Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
 Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available  
 at [http://www.sanger.ac.uk/projects/T\\_brucei/](http://www.sanger.ac.uk/projects/T_brucei/).

FEATURES  
 source  
 1..26  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
 /strain="TREU927"  
 /db\_xref="taxon:5691"  
 /clone="324D07"

Query Match 0.3%; Score 21.8; DB 1; Length 26;  
 Best Local Similarity 92.0%; Pred. No. 1.6e+02;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTCCTT 4488  
 Db 26 TTTT...TTTTCCTT 2

RESULT 111  
 AW327923/C 27 bp mRNA linear EST 28-JAN-2000  
 LOCUS dr02g08.x1 NIH\_MGC\_3 Homo sapiens cDNA clone IMAGE:2847159 5', mRNA  
 DEFINITION sequence.  
 ACCESSION AW327923  
 VERSION AW327923.1 GI:6798418  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 27)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
 cDNA Library Preparation: Edge Biosystems  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: NIH Intramural Sequencing Center (NISC)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Plate: LLCM0029 row: M column: 16  
 Seq primer: -21M13 forward primer (ABI).  
 Location/Qualifiers  
 1..27  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2847159"  
 /tissue\_type="Burkitt lymphoma"  
 /cell\_line="MGC4"  
 /clone\_lib="NIH\_MGC\_3"  
 /note="Organ: Lymph; Vector: pOTB7a; Library prepared by  
 Edge Biosystems."

Query Match 0.3%; Score 21.8; DB 1; Length 27;  
 Best Local Similarity 92.0%; Pred. No. 1.8e+02;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTCCTT 4488  
 Db 27 TTTT...TTTTCCTT 3

RESULT 112  
 CF291968 27 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14ROOT--02-J21.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
 DEFINITION sativa cDNA clone 14ROOT--02-J21, mRNA sequence.  
 ACCESSION CF291968  
 VERSION CF291968.1 GI:33661001  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 27)  
 Kim, J.S., Jun, K.W., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongui University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..27  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="14ROOT--02-J21"  
 /tissue\_type="root"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH108"  
 /clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
 /note="Vector: pCR4-TORO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 27;

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Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT...TTT 27 bp mRNA linear EST 15-AUG-2003
      ||||| 7LEAF--02-P02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
      1 TTTT...TTT 4488
      |||||
      25

RESULT 113
CF3299084 27 bp mRNA linear EST 15-AUG-2003
LOCUS 7LEAF--02-P02.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
DEFINITION sative cDNA clone 7LEAF--02-P02, mRNA sequence.
ACCESSION CF3299084
VERSION CF299084.1 GI:33670845
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--02-P02"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT...TTT 27 bp mRNA linear EST 18-AUG-2003
      ||||| NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
      1 TTTT...TTT 4488
      |||||
      25

RESULT 114
CF329725 27 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--05-C12.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sative cDNA clone NACL--05-C12, mRNA sequence.
ACCESSION CF329725
VERSION CF329725.1 GI:33807665
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

```

```

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--05-C12"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT...TTT 27 bp mRNA linear EST 18-AUG-2003
      ||||| NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
      1 TTTT...TTT 4488
      |||||
      25

RESULT 115
CF330557 27 bp mRNA linear EST 18-AUG-2003
LOCUS NACL--06-F04.b1 Rice callus plasmid cDNA library (NACL) Oryza
DEFINITION sative cDNA clone NACL--06-F04, mRNA sequence.
ACCESSION CF330557
VERSION CF330557.1 GI:33809352
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 27)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@bio.com, bnhnm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..27
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/clone="NACL--06-F04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```



Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Seq primer: m13 -40 forward  
High quality sequence stop: 1.

FEATURES  
source Location/Qualifiers  
1..27  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:3793948"  
/db\_xref="taxon:9606"  
/clone="IMAGE:244702"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal liver spleen lNfLS"  
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5'-AAGTCGAAGAATTAATAAGATCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

Query Match 0.3%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 88.5%; Pred.No.1.8e+02;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4465 TTTTGTCTTGGTCTTGA 4490  
|||||  
Db 1 TTTTGTCTTGGTCTTGA 26

RESULT 119  
N89936 27 bp mRNA linear EST 02-APR-1996  
LOCUS zB23e12.s1 Soares fetal lung NbHL19W Homo sapiens cDNA clone  
DEFINITION IMAGE:3029296 3' similar to gb:X59066 ATP SYNTHASE ALPHA CHAIN,  
MITOCHONDRIAL PRECURSOR (HUMAN); mRNA sequence.

ACCESSION N89936  
VERSION N89936.1 GI:1443263  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Hillier,L., Clark,N., Dubucque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le.M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasaki,E., Waterston,R., Williamson,A., Woldmann,P. and Wilson,R.  
TITLE The WashU-Merck EST Project  
JOURNAL Unpublished (1995)  
COMMENT Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: ET primer  
High quality sequence stop: 8.

FEATURES  
Location/Qualifiers  
1..27  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUCGCM0078H15"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Seq primer: ET primer  
High quality sequence stop: 1.

FEATURES  
source Location/Qualifiers  
1..27  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1247858"  
/db\_xref="taxon:9606"  
/clone="IMAGE:302926"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal lung NbHL19w"  
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCATTCTGAAGTGGAGCGCCCAATTTTTTTTTTTT 3], double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NbHL19w."

Query Match 0.3%; Score 21.8; DB 1; Length 27;  
Best Local Similarity 92.0%; Pred.No.1.8e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTTGGTCTT 4488  
|||||  
Db 3 TTTTGTCTTGGTCTT 27

RESULT 120  
AZ344642 27 bp DNA linear GSS 29-SEP-2000  
LOCUS IM0078H15R Mouse 10kb plasmid UUGCLM library Mus musculus genomic  
DEFINITION clone UUGCLM0078H15 R, genomic survey sequence.

ACCESSION AZ344642  
VERSION AZ344642.1 GI:10423879  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genomic Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0078 row: H column: 15  
Seq primer: CACACAGGAAACAGCATGACC  
Class: plasmid ends  
High quality sequence stop: 27.

FEATURES  
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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGCLM0078H15"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="vector: PWD42nv; Purified genomic DNA from *M. musculus* C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1|, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%; Score 21.8; DB 1; Length 27;
Best Local Similarity 92.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTTTGCTT 4488
Db 1 TTTTTTTTTTTTTTTTTTTTTTTTTT 25

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RESULT 122	AZ486791	LOCUS	AZ486791	27 bp	DNA	linear	GSS 05-OCT-2000
DEFINITION			1M0315K21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315K21 F, genomic survey sequence.				

VERSION	AZ486791.1	GI:10653911
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS	1 (bases 1 to 27)	
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb	

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: K column: 21  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 27.

FEATURES	source
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/organism="Mus musculus"	
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/strain="CS7BL/6J"	
/db_xref="taxon:10090"	
/clone="UUGC1M0315K21"	
/sex="Male"	
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"	
/clone_lib="Mouse 10kb plasmid UUGC1M library"	
/note="Vector: PWD42nb; Purified genomic DNA from M."	

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1. 27
source
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0369E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

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musculus C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA

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FEATURES
source
High quality sequence stop: 27.
Location/Qualifiers
1. 27
/organism="Mus musculus"

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laboratory mouse DNA resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a







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RESULT 135
CF330938/c
LOCUS       CF330938             28 bp      mRNA      linear      EST 18-AUG-2003
DEFINITION  NACL--06-N19.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--06-N19, mRNA sequence.
ACCESSION   CF330938
VERSION     CF330938.1
KEYWORDS    GI:33810102
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
     source           1..28
                     /organism="Oryza sativa"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:4530"
                     /clone="NACL--06-N19"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 30 days"
                     /lab_host="E.coli DH10B"
                     /clone_lib="Rice callus plasmid cDNA library (NACL)"
                     /notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                     with oligoribonucleotides and then used as templates for
                     RT-PCR."

Query Match      0.3%;   Score 21.8;   DB 1;   Length 28;
Best Local Similarity 92.0%;   Pred. No. 2e+02;
Matches 23;   Conservative 0;   Mismatches 2;   Indels 0;   Gaps 0;

Qy      4464  TTTTGTGTTTTTTTTTTTGTGCTT 4488
Db      28    TTTTGTGTTTTTTTTTTTGTGCTT 4

RESULT 136
AZ399637/c
LOCUS       AZ399637             28 bp      DNA      linear      GSS 03-OCT-2000
DEFINITION  clone UUGC1M0165N04 R, genomic survey sequence.
ACCESSION   AZ399637
VERSION     AZ399637.1
KEYWORDS    GI:10514711
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 28)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D. Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center

```









Insert Length: 10000 Std Error: 0.00

plate: 0099 row: D column: 0000







**AZ389566/c**  
**LOCUS** 29 bp DNA linear GSS 02-OCT-2000  
**DEFINITION** IM0150D2lf Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 clone UGCG1M0150D21 F, genomic survey sequence.  
**ACCESSION**  
**VERSION** AZ389566  
**KEYWORDS** AZ389566.1 GI:10503274  
**SOURCE** GSS.  
**ORGANISM** Mus musculus (house mouse)  
**REFERENCE** Mus musculus  
**AUTHORS** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 29)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Irlam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0150 row: D column: 21  
 Seq primer: CGTGTGAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 29.  
 Location/Qualifiers

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Query Match      0.3%; Score 21.8; DB 1; Length 29;
Best Local Similarity 92.0%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464 TTTTTTTTTTTTTTTTTTTTGTCTT 4488
Db       29 TTTTTTTTTTTTTTTTTTTTTTTTTTTT 5

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RESULT 153  
AZ414283

LOCUS	29 bp	DNA	linear	GSS 03-OCT-2000
DEFINITION	1M0188G12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0188G12 R, genomic survey sequence.			
ACCESSION	AZ414283			
VERSION	AZ414283.1			
KEYWORDS	GSS			
SOURCE	AZ414283.1 GI:10538296			
ORGANISM	Mus musculus (house mouse)			
REFERENCE	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 29)			
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,S., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0198 row: G column: 12 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 29. Location/Qualifiers 1..29			
FEATURES				
	source			

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Query Match      0.3%; Score 21.8; DB 1; Length 29;
Best Local Similarity 92.0%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4464 TTTTTTTTTTTTTTTTTTTTGTCTT 4488
Db      1 TTTTTTTTTTTTTTTTTTTTTTTTTTTT 25

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RESULT 154  
AZ451930  
LOCUS

29 bp DNA linear GSS 04-OCT-2000

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DEFINITION      1M0251E05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0251E05 R, genomic survey sequence.
ACCESSION       AZ451930
VERSION         AZ451930
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
REFERENCE
AUTHORS         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE           Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL         Unpublished (2000)
COMMENT         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0251 row: E column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 29.
FEATURES        Location/Qualifiers
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                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0251E05"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
                Query Match      0.3%; Score 21.8; DB 1; Length 29;
                Best Local Similarity 92.0%; Pred. No. 2.1e+02;
                Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464  TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db      1      TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 155
AZ468402
LOCUS      AZ468402
DEFINITION 1M0281G24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0281G24 F, genomic survey sequence.
ACCESSION       AZ468402
VERSION         AZ468402
KEYWORDS        GSS.
SOURCE          Mus musculus (house mouse)
ORGANISM        Mus musculus
REFERENCE
AUTHORS         Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
TITLE           Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL         Unpublished (2000)
COMMENT         Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0281 row: G column: 24
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
FEATURES        Location/Qualifiers
source          1..29
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0281G24"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adaptor DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adaptor mouse DNA was annealed to
                adaptor vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
                Query Match      0.3%; Score 21.8; DB 1; Length 29;
                Best Local Similarity 92.0%; Pred. No. 2.1e+02;
                Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4464  TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db      1      TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 156
AZ486793
LOCUS      AZ486793
DEFINITION 1M0315N21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315N21 F, genomic survey sequence.

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ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 FEATURES  
 source

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A2486793
A2486793.1 GI:10653915
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 29)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Stokes,R., Tingley,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., StC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: N column: 21
Seq primer: CGTTGTAAACAGCGGCCAGT
Class: plasmid ends
High quality sequence stop: 29.
Location/Qualifiers
1..29
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="UUGC1M0315N21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pPWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.3%; Score 21.8; DB 1; Length 29;
Best Local Similarity 92.0%; Pred. No. 2.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTTTGCTT 4488
|||||||
Db 1 TTTTTTTTTTTTTTTTTTTTTTTT 25

RESULT 157
A2661709
LOCUS
DEFINITION
Accession
A2661709
IM0540K20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0540K20 F, genomic survey sequence.
ACCESSION
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**KEYWORDS**  
SOURCE Mus musculus (house mouse)  
**ORGANISM**  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE**  
AUTHORS 1 (bases 1 to 29)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,S., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Stokes,R., Tingley,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
**JOURNAL**  
Unpublished (2000)  
**COMMENT**  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0026 row: I column: 13  
Seq primer: CACACGAGAACACTATGACC  
Class: plasmid ends  
High quality sequence stop: 29.  
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/db\_xref="taxon:10090"  
/clone="UUGC2M0026I13"  
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/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptored DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptored mouse DNA was annealed to  
adaptored vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match	0.3%; Score 21.8; DB 1;	Length 29;
Best Local Similarity	92.0%; Pred.No.2.le+07;	
Matches 23;	Conservative 0; Mismatches 2;	Indels 0; Gaps 0;

QY 4464 TTTTNTTTTTTTTTTTTTTTTTTGCTT 4488  
|||||||  
Db 29 TTTTNTTTTTTTTTTTTTTTTTTTTTT 5

RESULT 159  
AZ806470/c  
LOCUS AZ806470 29 bp DNA linear GSS 20-FEB-2001  
DEFINITION 2M0068102R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
Clone UUGC2M0068102 R, genomic survey sequence.  
ACCESSION AZ806470  
VERSION AZ806470.1 GI:12969849  
KEYWORDS GSS.



ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE AUTHORS	1 (bases 1 to 29) Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL COMMENT	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: <a href="mailto:rdunn@genetics.utah.edu">rdunn@genetics.utah.edu</a> Insert Length: 10000 Std Error: 0.00 Plate: 0078 row: J column: 15 Seq primer: CACACGAGAAACAGCTATGACC Class: plasmid ends High quality sequence stop: 29. Location/Qualifiers

FEATURES	SOURCE
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Location/Qualifiers	
/organism="Mus musculus"	
/mol_type="genomic DNA"	
/strain="C57BL/6J"	
/db_xref="taxon:10090"	
/clone="UUCG2M0078J15"	
/sex="Male"	
/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"	
/clone_lib="Mouse 10kb plasmid UUCG1M library"	
/note="Vector: pWP42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource ( <a href="http://www.jax.org/resources/documents/dnares/">http://www.jax.org/resources/documents/dnares/</a> ). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (gil4732114[gb AF129072.1]), a copy-number ligated inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent <i>E. coli</i> XL10-Gold (Stratagene) cells and selected for ampicillin resistance."	

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Query Match      0.1%; Score 21.8; DB 1;  Lengun 29;
Best Local Similarity 92.0%; Pred. NO. 2.1e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTTTTTTTTTTTTTTTTTTTTTTGTCTT 4488
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Db 29 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 5

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RESULT	161
LOCUS	AZ868731/c
DEFINITION	29 bp DNA linear GSS 21-FEB-2001 2M018010J2R Mouse 10kb plasmid UUGCIM library Mus.musculus genomic clone UUGC2M0180L02 R, genomic survey sequence.
ACCESSION	AZ868731
VERSION	AZ868731.1
KEYWORDS	GI:13072338, GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases:1 to 29)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
Rm. 308, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0180 row: L column: 02  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
which quality sequence stop: 29.

## FEATURES

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1. .23
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0180L02"
/sex="Male"
/lab_host="E. Coli strain"
/clone_lib="Mouse 10kb p
/notes="Vector: PWD42nv;
musculus C57BL/6J (male)
Laboratory Mouse DNA Res
(http://www.jax.org/resc
was hydrodynamically sheared
0.005 inch orifice at co
was blunt end-repaired v
polynucleotide kinase. I
ligated to the blunt end
adapted DNA was purifi
10.5 kb range using pre
electrophoresis. Vector
of PWD42 [gi|4732114|gb
inducible derivative of
with adaptors compleme
purified. The sheared, a
adapted vector DNA, a
chemically-competent E.
and selected for ampic

```

	Query Match	0.3%	Score 21.8;	DB 1;	Length 29;
Best Local Similarity	92.0%		Pred. No. 2.1e+02;		
Matches 23; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	4464	TTTTTTTTTTTTTTTTTTTTTTCTCTT	4488		
nb	29	TTTTTTTTTTTTTTTTTTTTTTTTTTTT	5		

RESULT 162	TA334G09Q	29 bp	DNA	linear	GSS 13-DEC-2000			
LOCUS	TA334G09Q	T. brucei sheared genomic DNA clone 334g09, reverse sequence,						
DEFINITION	genomic survey sequence.							
ACCESSION	AL491938							
VERSION	AL491938.1	GI:11868238						
KEYWORDS	GSS.							
SOURCE	Trypanosoma brucei							
ORGANISM	Trypanosoma brucei							
	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;							









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Query Match      0.3%; Score 21.8; DB 1; Length 30;
Best Local Similarity 92.0%; Pred. No. 2.3e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT... 4488
DB 25 TTTT... 1

RESULT 173
AZ455741/c
LOCUS
DEFINITION
  1M0258D16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0258D16 F, genomic survey sequence.
ACCESSION
  AZ455741
VERSION
  AZ455741.1 GI:10613866
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 30)
REFERENCE
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0258 row: D column: 16
  Seq primer: CGTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 30.
  Location/Qualifiers
    1..30
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0258D16"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptor DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptor mouse DNA was annealed to
      adaptor vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."

FEATURES
  source
    1..30
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0258D16"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /note="Vector: PWD42nv; Purified genomic DNA from M.
      musculus C57BL/6J (male) was obtained from the Jackson
      Laboratory Mouse DNA Resource
      (http://www.jax.org/resources/documents/dnares/). The DNA
      was hydrodynamically sheared by repeated passage through a
      0.005 inch orifice at constant velocity. The sheared DNA
      was blunt end-repaired with T4 DNA polymerase and T4
      polynucleotide kinase. Adaptor oligonucleotides were
      ligated to the blunt ends in high molar excess. The
      adaptor DNA was purified and size-selected for a 9.5 to
      10.5 kb range using preparative agarose gel
      electrophoresis. Vector DNA was prepared from a derivative
      of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
      inducible derivative of plasmid R1. The vector was ligated
      with adaptors complementary to the insert adaptors and
      purified. The sheared, adaptor mouse DNA was annealed to
      adaptor vector DNA, and transformed into
      chemically-competent E. coli XL10-Gold (Stratagene) cells
      and selected for ampicillin resistance."

```

Best Local Similarity 92.0%; Pred. No. 2.3e+02; Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT... 4488  
Db 1 TTTT... 25

RESULT 175  
LOCUS AZ582114 30 bp DNA linear GSS 13-DEC-2000  
DEFINITION LM0374J17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0374J17 F, genomic survey sequence.

ACCESSION AZ582114  
VERSION AZ582114.1 GI:11700674  
KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 30)

AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
Fax: 801 585 7177

Email: dunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0374 row: J column: 17

Seq primer: CTTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 30.

Location/Qualifiers

1..30  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0374J17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

FEATURES  
source

Query Match 0.3%; Score 21.8; DB 1; Length 30;  
Best Local Similarity 92.0%; Pred. No. 2.3e+02;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT... 4488  
Db 1 TTTT... 25

RESULT 176

LOCUS AW249485 31 bp mRNA linear EST 07-JAN-2000

DEFINITION 2821429.3prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821429 3',  
mRNA sequence.

ACCESSION AW249485

VERSION AW249485.1 GI:6592478

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 31)

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Other ESTs: 2821429.5prime  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/BTP cDNA Library Preparation: Ling  
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing  
project Clone distribution: MGC clone distribution information can  
be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality  
Scores: PHRED from University of Washington Genome Center  
Trimming: cross match from University of Washington Genome Center  
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley  
Drosophila Genome Project. University of Washington Genome Center:  
http://www.genome.washington.edu Low Quality Sequence: 20  
contiguous PHRED high quality bases following vector sequence. Very  
Low Quality Sequence: Trace file contained 31 contiguous distinct  
peaks following vector sequence. Polyadenylation: Based upon the  
presence of a XhoI site followed by a run of 14 or more T residues  
at the beginning of the sequence, this cDNA insert was  
polyadenylated.

High quality sequence stop: 20.

Location/Qualifiers

1..31  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821429"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GCACGAG(G). Size-selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

Query Match 0.3%; Score 21.8; DB 1; Length 31;  
Best Local Similarity 92.0%; Pred. No. 2.5e+02;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT... 4488  
Db 4 TTTT... 28

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RESULT 177
BX569502
LOCUS      BX569502 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse9a03_plc, mRNA sequence.
ACCESSION  BX569502
VERSION     BX569502.1 GI:33437420
KEYWORDS    EST.
SOURCE      Glossina morsitans morsitans
ORGANISM    Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscidae; Glossinidae; Glossina.
REFERENCE   1 (bases 1 to 31)
AUTHORS     Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
            Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE       Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
JOURNAL     Genome Biol. 4 (10), R63 (2003)
MEDLINE     22881942
PUBMED      14519198
COMMENT     Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxton, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J. Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all plc reads are from
            the 3' end.

FEATURES             source
            Location/Qualifiers
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                /organism="Glossina morsitans morsitans"
                /mol_type="mRNA"
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                /db_xref="taxon:37546"
                /clone="Tse9a03_plc"
                /tissue_type="adult infected gut"
                /clone_lib="Glossina morsitans morsitans adult infected
                gut"
                /note="country: Zimbabwe; EST from adult gut infected with
                T.brucei"

Query Match      0.3%; Score 21.6; DB 1; Length 31;
Best Local Similarity 92.0%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db      1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 178
CF278807/c
LOCUS      CF278807 31 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--04-N15.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
ACCESSION  CF278807
VERSION     CF278807.1 GI:33656193
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 31)
AUTHORS     Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs

Query Match      0.3%; Score 21.6; DB 1; Length 31;
Best Local Similarity 92.0%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db      1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 179
CF278807/c
LOCUS      CF278807 31 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-L08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION  CF278807
VERSION     CF278807.1 GI:33672106
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 31)
AUTHORS     Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Gyeonggi, Korea
            Tel: 82 31 321 6193
            Fax: 82 31 321 6355
            Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
            Location/Qualifiers
                1..31
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                /cultivar="Nackdong"
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                /clone="14ETL--04-N15"
                /tissue_type="leaf"
                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice etiolated leaf plasmid cDNA library
                (14ETL)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.3%; Score 21.8; DB 1; Length 31;
Best Local Similarity 92.0%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db      31 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 179
CF300345
LOCUS      CF300345 31 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--04-L08.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION  CF300345
VERSION     CF300345.1 GI:33672106
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 31)
AUTHORS     Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
            Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Gyeonggi, Korea
            Tel: 82 31 321 6193
            Fax: 82 31 321 6355
            Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

FEATURES             source
            Location/Qualifiers
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                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="7LEAF--04-L08"
                /tissue_type="leaf"
                /dev_stage="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

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RESULT 180
AZ333315      31 bp      DNA      linear      GSS 29-SEP-2000
LOCUS      1M0062A21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0062A21 F, genomic survey sequence.
ACCESSION      AZ333315
VERSION      AZ333315.1 GI:10397811
KEYWORDS
SOURCE      GSS.
            Mus musculus (house mouse)
ORGANISM      Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 31)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0062 row: A column: 21
            Seq primer: CGTGTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES
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            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0062A21"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

RESULT 181
AZ375973      31 bp      DNA      linear      GSS 02-OCT-2000
LOCUS      1M0129D08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION      clone UUGC1M0129D08 R, genomic survey sequence.
ACCESSION      AZ375973
VERSION      AZ375973.1 GI:10489673
KEYWORDS
SOURCE      GSS.
            Mus musculus (house mouse)
ORGANISM      Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 31)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL
COMMENT      Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0129 row: D column: 08
            Seq primer: CACACAGGAAACACGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 31.
FEATURES
            source
            1..31
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0129D08"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

Query Match      0.3%; Score 21.8; DB 1; Length 31;
Best Local Similarity      92.0%; Pred. No. 2.5e+02;

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Query Match          0.3%; score 21.6; DB 1; length 31;
Best Local Similarity 92.0%; Pred. No. 2.5e+02;

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/mol_type="Genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0014002"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGClm library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male); Was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnareg/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptorised mouse DNA was annealed to adaptorised vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
Query Match      0.3%; Score 21.8; DB 1; Length 31;
Best Local Similarity 92.0%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
4464 TTTT TTTTTT TTTTTT TTTTTCCT 4488
|||||

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CA). Note: this is a NIH\_MGC Library."

Query Match 0.3%; Score 21.8; DB 1; Length 32;  
Best Local Similarity 92.0%; Pred. No. 2.7e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTTCTTTTCTTTTCTTTGCTTTG 4489  
DB 32 TTTTCTTTTCTTTTCTTTTCTTTT 8

RESULT 191  
CF291773  
LOCUS CF291773 32 bp mRNA linear EST 14-AUG-2003  
DEFINITION 14ROOT--02-F12.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
sativa cDNA clone 14ROOT--02-F12, mRNA sequence.  
ACCESSION CF291773  
VERSION CF291773.1 GI:33660806  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
source  
1..32  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ROOT--02-F12"  
/tissue\_type="root"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 32;  
Best Local Similarity 92.0%; Pred. No. 2.7e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTTT 4488  
DB 1 TTTTCTTTTCTTTTCTTTTCTTTT 25

RESULT 192  
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LOCUS CF299386 32 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF--03-G07.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--03-G07, mRNA sequence.  
ACCESSION CF299386  
VERSION CF299386.1 GI:33671147  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
source  
1..32  
/organism="Oryza sativa"  
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/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 32;  
Best Local Similarity 92.0%; Pred. No. 2.7e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTTT 4488  
DB 1 TTTTCTTTTCTTTTCTTTTCTTTT 25

RESULT 193  
CF309233/c  
LOCUS CF309233 32 bp mRNA linear EST 15-AUG-2003  
DEFINITION ABF--03-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--03-F14, mRNA sequence.  
ACCESSION CF309233  
VERSION CF309233.1 GI:33680994  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 32)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
source  
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/organism="Oryza sativa"  
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/cultivar="Nackdong"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"



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/organism="Oryza sativa"
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/cultivar="Nackdong"
/db_xref="taxon:4530"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH108"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 197
CF321046
LOCUS
DEFINITION
HD--12-C15-g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--12-C15, mRNA sequence.
ACCESSION
CF321046
VERSION
CF321046.1 GI:33692807
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)
/lab_host="E.coli DH108"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 32
/organism="Oryza sativa"
/mol_type="mRNA"
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/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 199
CF331270
LOCUS
DEFINITION
NACL--07-F08-b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-F08, mRNA sequence.
ACCESSION
CF331270
VERSION
CF331270.1 GI:33810751
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)
/lab_host="E.coli DH108"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488

```

```

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 198
CF328471
LOCUS
DEFINITION
NACL--03-G09-b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--03-G09, mRNA sequence.
ACCESSION
CF328471
VERSION
CF328471.1 GI:33805189
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)
/lab_host="E.coli DH108"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 32
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="NACL--03-G09"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 25

RESULT 199
CF331270
LOCUS
DEFINITION
NACL--07-F08-b1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--07-F08, mRNA sequence.
ACCESSION
CF331270
VERSION
CF331270.1 GI:33810751
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 32)
/lab_host="E.coli DH108"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 21.8; DB 1; Length 32;
Best Local Similarity 92.0%; Pred. No. 2.7e+02;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4488

```



schultz078-3.rst

Thu Oct 14 15:43:37 2004

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 21.8; DB 1; Length 32;  
Best Local Similarity 92.0%; Pred. NO. 2.7e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTTGTCTT 4488  
DB 1 TTTTGTCTTGTCTT 25

RESULT 201

AZ470832/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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1..32

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0285F14"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

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musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnamh@bio.com, bnamh@bio.myongji.ac.kr.  
Location/Qualifiers  
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/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="NACL-07-F08"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 30 days"  
/lab\_host="E. coli DH10B"  
/clone\_lib="Rice callus plasmid cDNA library (NACL)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 32;  
Best Local Similarity 92.0%; Pred. NO. 2.7e+02;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTGTCTTGTCTT 4488  
DB 1 TTTTGTCTTGTCTT 25

RESULT 200

AZ459536

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0264M16"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

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musculus C57BL/6J (male) was obtained from the Jackson

musculus C57BL/6J (male) was obtained from the Jackson

Km. 306, Biomeuclida Polymers Research Bldg., 40 S. 2030 E., SLU, U.  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0012 row: 0 column: 20  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 32.  
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 /db\_xref="taxon:10090"  
 /clone="UUGC2M0012020"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCJM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources>). The DNA

RESULT 205  
BU431798  
LOCUS  
DEFINITION  
33 bp mRNA linear EST 09-SEP-2002  
601655890R1 NIH\_MCC\_66 Homo sapiens cDNA clone IMAGE:3855694 3',  
mRNA sequence.  
BU431798  
ACCESSION  
BU431798.1 GI:22770280  
KEYWORDS  
EST.

All clones with suffix qic are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

#### FEATURES

source Location/Qualifiers  
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 /organism="Glossina morsitans morsitans"  
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 /clone\_lib="Tse36g10 plc"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 21.8; DB 1; Length 33;  
 Best Local Similarity 92.0%; Pred. No. 2.9e+02;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4462 ACATTTTCTTTTCTTTTCTTCTC 4486  
 TTTTCTTTTCTTTTCTTTTCTTTTCTTCTC 33  
 Db 9 AGTTTCTTTTCTTTTCTTTTCTTTTCTTCTC 33

#### RESULT 207

CF291613 33 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14ROOT--02-B21.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
 DEFINITION sativa cDNA clone 14ROOT--02-B21, mRNA sequence.

ACCESSION CF291613  
 VERSION CF291613.1 GI:33660646  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 33)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.myongji.ac.kr.

#### FEATURES

source Location/Qualifiers  
 1. .33  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="14ROOT--02-B21"  
 /tissue\_type="root"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 21.8; DB 1; Length 33;  
 Best Local Similarity 92.0%; Pred. No. 2.9e+02;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTCTC 4488  
 TTTTCTTTTCTTTTCTTTTCTTTTCTTCTC 25  
 Db 1 TTTTCTTTTCTTTTCTTTTCTTTTCTTCTC 25

#### RESULT 208

CF311229 33 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--06-F23.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (ABF) Oryza sativa cDNA clone ABF--06-F23, mRNA sequence.

ACCESSION CF311229  
 VERSION CF311229.1 GI:33682990  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 33)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.myongji.ac.kr.

#### FEATURES

source Location/Qualifiers  
 1. .33  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="ABF--06-F23"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 21.8; DB 1; Length 33;  
 Best Local Similarity 92.0%; Pred. No. 2.9e+02;  
 Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTCTC 4488  
 TTTTCTTTTCTTTTCTTTTCTTTTCTTCTC 25  
 Db 1 TTTTCTTTTCTTTTCTTTTCTTTTCTTCTC 25

#### RESULT 209

CF326967 33 bp mRNA linear EST 18-AUG-2003  
 LOCUS NACL--01-E04.b1 Rice callus plasmid cDNA library (NACL) Oryza  
 DEFINITION sativa cDNA clone NACL--01-E04, mRNA sequence.

ACCESSION CF326967  
 VERSION CF326967.1 GI:33802189  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 33)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division







```

QY      4464  TTTT...TTTGTCTTGAGAC 4493
Db      31  TTTT...TTTGTCTTGAGAC 2

RESULT 217
AZ425710/c
LOCUS   AZ425710
DEFINITION  23 bp DNA linear GSS 03-OCT-2000
clone UUGC1M0205L23 R, genomic survey sequence.
ACCESSION  AZ425710
VERSION     A2425710.1 GI:10549723
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 23)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu

            Insert Length: 10000 Std Error: 0.00
            Plate: 0205 row: L column: 23
            Seq primer: CACACAGGAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES             Location/Qualifiers
     source           1..23
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0205L23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of PWD42 (gil4732114[gb|AF129072.1]), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

Query Match      0.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```

```

QY      4464  TTTT...TTTGTCTTGAC 4486
Db      23  TTTT...TTTGTCTTGAC 1

RESULT 218
AL048765/c
LOCUS   AL048765
DEFINITION  24 bp mRNA linear EST 04-SEP-2003
DKFP566M233_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
DKFP566M233, mRNA sequence.
ACCESSION  AL048765
VERSION     AL048765.1 GI:4727836
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE       EST (Koehrer, et al.)
JOURNAL     Unpublished (1999)
COMMENT     Contact: MIPS
            MIPS
            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES             Location/Qualifiers
     source           1..24
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="DKFP566M233"
                     /tissue_type="kidney"
                     /dev_stage="fetal"
                     /lab_host="Xl-2blue"
                     /clone_lib="566 (synonym: hfkd2)"
                     /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match      0.3%; Score 21.4; DB 1; Length 24;
Best Local Similarity 95.7%; Pred. No. 1.6e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


```

```

QY      4464  TTTT...TTTGTCTTGAC 4486
Db      24  TTTT...TTTGTCTTGAC 2

RESULT 219
AZ812579/c
LOCUS   AZ812579
DEFINITION  24 bp DNA linear GSS 20-FEB-2001
clone UUGC2M0079A23 F, genomic survey sequence.
ACCESSION  AZ812579
VERSION     AZ812579.1 GI:12981965
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu

Query Match      0.3%; Score 21.4; DB 1; Length 23;
Best Local Similarity 95.7%; Pred. No. 1.4e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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Qy 4464 TTTTCTTTTCTTTTCTTTTGTGTC 4486  
 |||||  
 Db 2 TTTTCTTTTCTTTTCTTTTCTTTTCTT 24

RESULT 224  
 A2941721  
 LOCUS 27 bp DNA linear GSS 26-APR-2001  
 DEFINITION 2M0201004R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0201004 R, genomic survey sequence.  
 ACCESSION A2941721  
 VERSION A2941721.1 GI:13804440  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 27)  
 REFERENCE  
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0201 row: 0 column: 04  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 FEATURES  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0201004"  
 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57Bl/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 21.4; DB 1; Length 27;  
 Best Local Similarity 95.7%; Pred. No. 2.1e+02;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4463 CTTTCTTTTCTTTTCTTTTGTGT 4485  
 |||||  
 Db 4 CTTTCTTTTCTTTTCTTTTGTGT 26

RESULT 225  
 AL587582  
 LOCUS 28 bp mRNA linear EST 02-MAR-2001  
 DEFINITION AL587582 BP Chicken Brain Library Gallus gallus cDNA clone  
 ROS059D03, mRNA sequence.  
 ACCESSION AL587582  
 VERSION AL587582.1 GI:13192616  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 28)  
 REFERENCE  
 AUTHORS Murray, F.  
 TITLE BP Chicken Brain Library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Frazer Murray  
 Dept. Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UK  
 Tel: +44 (0)131 527 4200  
 Fax: +44 (0)131 440 0434  
 Email: frazer.murray@bbsrc.ac.uk  
 GCGGCGCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from Clonetechn  
 (\*6854-)  
 Seq primer: M13F.  
 FEATURES  
 Location/Qualifiers  
 1..28  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="ROS059D03"  
 /tissue\_type="Brain"  
 /dev\_stage="Unknown"  
 /lab\_host="DH10B"  
 /clone\_lib="BP Chicken Brain Library"  
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned  
 unidirectionally. Primer: Oligo dt. 5' adaptor sequence:  
 5' TCGACCTCTGAG 3' ; 3' adaptor sequence: 5'  
 GCGGCGCTTTTCTTTTCTTTTCTTTT 3' Poly A RNA purchased from  
 Clonetechn (\*6854-1)"

Query Match 0.3%; Score 21.4; DB 1; Length 28;  
 Best Local Similarity 95.7%; Pred. No. 2.3e+02;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTTGTGTC 4486  
 |||||  
 Db 6 TTTTCTTTTCTTTTCTTTTGTGTC 28

RESULT 226  
 AL048684/c  
 LOCUS 30 bp mRNA linear EST 04-SEP-2003  
 DEFINITION AL048684 DXF2p566C043 r1 566 (synonym: hfkcd2) Homo sapiens cDNA clone  
 DXF2p566C043, mRNA sequence.  
 ACCESSION AL048684  
 VERSION AL048684.1 GI:4727755  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 30)  
 REFERENCE  
 AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
 TITLE EST (Koehrer, et al.)  
 JOURNAL Unpublished (1999)

Query Match 0.3%; Score 21.4; DB 1; Length 27;  
 Best Local Similarity 95.7%; Pred. No. 2.1e+02;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



SOURCE	Beta vulgaris
ORGANISM	Beta vulgaris
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.

```

REFERENCE
AUTHORS      1 (bases 1 to 27)
              Herwig,R., Schulz,B., Weigshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,W., Stal,D., Wuck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weishaar B
              ADIS DNA core facility at MPIZ
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weishaar@mpiz-koeln.mpg.de
              Insert Length: 27 Std Error: 0.00
              Plate: 17 row: L column: 16
              Seq primer: T7; GTAATACGACTCACTATAGGC.

FEATURES
source       1..27
              /organism="Beta vulgaris"
              /mol_type="mRNA"
              /cultivar="KWS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:188934"
              /db_xref="taxon:161934"
              /clone="024-017-Li6"
              /tissue_type="storage root"
              /lab_host="EMDH10B"
              /clone_lib="MPI2-ADIS-024-storage root"
              /note="Vector: PCWSP0T6; Site 1: SalI; Site 2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinzanlebener Saat-zucht AG Einbeck, Germany, contact:
              b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
              orientation:
              SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 21.2; DB 1; Length 27;
Best Local Similarity 88.5%; Pred. No. 2.3e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4466 TTTTGTGTTTTTTTGTCTTGAG 4491
Db 1 TTTTGTGTTTTTTTGTCTTGAG 26

RESULT 233
R37697
LOCUS       R37697      28 bp      mRNA      linear      EST 04-MAY-1995
DEFINITION yf50c03.s1 Soares infant brain INIB Homo sapiens cDNA clone
IMAGE:25521 3' similar to gb:J03040 SPARC PRECURSOR (HUMAN);, mRNA
sequence.
ACCESSION   R37697
VERSION     R37697.1 GI:795153
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Hallier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
            Wilson,R.
            The WashU-Merck EST Project
            Unpublished (1995)
            Contact: Wilson RK
            Washington University School of Medicine

Query Match      0.3%; Score 21.2; DB 1; Length 28;
Best Local Similarity 85.2%; Pred. No. 2.5e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4465 TTTTGTGTTTTTTTGTCTTGAG 4491
Db 1 TTTTGTGTTTTTTTGTCTTGAG 27

RESULT 234
R37697
LOCUS       AZ358038/c 28 bp      DNA      linear      GSS 02-OCT-2000
DEFINITION clone UUGCIM0100F05 F, genomic survey sequence.
ACCESSION   AZ358038
VERSION     AZ358038.1 GI:10471738
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 28)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
            Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
            Unpublished (2000)
            Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0100 row: F column: 05
            Seq primer: CGTTGTAAAAACGACGCCAGT

```

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Insert Size: 1410  
 High quality sequence starts: 1 High quality sequence stops: 1  
 Source: IMAGE Consortium, LLNL This clone is available royalty-free  
 through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)  
 for further information. Trace considered overall poor quality  
 Insert Length: 1410 Std Error: 0.00  
 Seq primer: -21ml3  
 High quality sequence stop: 1.

#### FEATURES

source

1..28  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="GDB:397868"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:25521"  
 /sex="female"  
 /dev\_stage="73 days post natal"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares infant brain INIB"  
 /note="Organ: whole brain; Vector: Lafmid BA; Site 1: Not  
 I; Site 2: Hind III; 1st strand cDNA was primed with a Not  
 I - oligo(dT) primer [5,  
 AACTGGAGAAATTCGGCGCGAGGAATTTTTTTTTTTT 3'];  
 double-stranded cDNA was ligated to Hind III adaptors  
 (Pharmacia), digested with Not I and directionally cloned  
 into the Not I and Hind III sites of the Lafmid BA vector.  
 Library went through one round of normalization. Library  
 constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 0.3%; Score 21.2; DB 1; Length 28;  
 Best Local Similarity 85.2%; Pred. No. 2.5e+02;  
 Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Qy 4465 TTTTGTGTTTTTTTGTCTTGAG 4491  
 Db 1 TTTTGTGTTTTTTTGTCTTGAG 27

RESULT 234  
 R37697  
 LOCUS AZ358038/c 28 bp DNA linear GSS 02-OCT-2000  
 DEFINITION clone UUGCIM0100F05 F, genomic survey sequence.  
 ACCESSION AZ358038  
 VERSION AZ358038.1 GI:10471738  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0100 row: F column: 05  
 Seq primer: CGTTGTAAAAACGACGCCAGT

```

index: 0074  row: 0  column: 14
seq primer: GGTGTAAACGACGGCCAGT
Class: plasmid ends
/dev_stage= young adult
/clone_lib="Nori satcho unpublished cDNA library, young
adult"

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Query Match      0.3%; Score 21.2; DB 1; Length 31;
Best Local Similarity 85.2%; Pred. No. 3.2e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTTGT 4485
Db 5 TCGAGTTTTTTTTTTTTTTTTTTTTCGT 31

RESULT 237
BX551460
LOCUS
DEFINITION BX551460 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone fse118902_plc, mRNA sequence.
ACCESSION BX551460
VERSION BX551460.1 GI:33375626
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="fse1b01_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match      0.3%; Score 21.2; DB 1; Length 32;
Best Local Similarity 88.5%; Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4460 GGACTTTTTTTTTTTTTTTTTTTTGT 4485
Db 6 GGTCTTTTTTTTTTTTTTTTTTTT 31

RESULT 239
BX555533
LOCUS
DEFINITION BX555533 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse21c01_plc, mRNA sequence.
ACCESSION BX555533
VERSION BX555533.1 GI:33379519
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit

```

```

KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix g1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..32
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="fse1b01_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match      0.3%; Score 21.2; DB 1; Length 32;
Best Local Similarity 88.5%; Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4460 GGACTTTTTTTTTTTTTTTTTTTTGT 4485
Db 6 GGTCTTTTTTTTTTTTTTTTTTTT 31

RESULT 239
BX555533
LOCUS
DEFINITION BX555533 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse21c01_plc, mRNA sequence.
ACCESSION BX555533
VERSION BX555533.1 GI:33379519
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 32)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit

```



The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

#### FEATURES source

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1..32      Location/Qualifiers
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /sub_species="morsitans"
            /db_xref="taxon:37546"
            /clone="Tse21c01_plc"
            /tissue_type="adult infected gut"
            /clone_lib="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucei"
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Query Match 0.3%; Score 21.2; DB 1; Length 32;  
Best Local Similarity 88.5%; Pred. No. 3.4e+02;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4484  
Db 4 TAGAAGTTTTTTTTTTTTTTTTTTTG 29

RESULT 240 BX558102 32 bp mRNA linear EST 10-OCT-2003  
LOCUS BX558102 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse36f08\_plc, mRNA sequence.

ACCESSION BX558102  
VERSION BX558102.1 GI:33429249  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerkhoun,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

#### FEATURES source

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1..32      Location/Qualifiers
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /sub_species="morsitans"
            /db_xref="taxon:37546"
            /clone="Tse36f08_plc"
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/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.3%; Score 21.2; DB 1; Length 32;  
Best Local Similarity 88.5%; Pred. No. 3.4e+02;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4458 ATGACATTTTTTTTTTTTTTTTTTTT 4483  
Db 7 ATAGTTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 241 BX560723 32 bp mRNA linear EST 10-OCT-2003  
LOCUS BX560723 Glossina morsitans morsitans adult infected gut Glossina  
DEFINITION morsitans morsitans cDNA clone Tse50g08\_plc, mRNA sequence.

ACCESSION BX560723  
VERSION BX560723.1 GI:33369704  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerkhoun,A., Berriman,M.,  
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

#### FEATURES source

```
1..32      Location/Qualifiers
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /sub_species="morsitans"
            /db_xref="taxon:37546"
            /clone="Tse50g08_plc"
            /tissue_type="adult infected gut"
            /clone_lib="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucei"
```

Query Match 0.3%; Score 21.2; DB 1; Length 32;  
Best Local Similarity 88.5%; Pred. No. 3.4e+02;  
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4458 ATGACATTTTTTTTTTTTTTTTTTTT 4483  
Db 7 ATAGTTTTTTTTTTTTTTTTTTTTTTT 32

RESULT 242  
BX564047

LOCUS	32 bp	linear	EST 10-OCT-2003
DEFINITION	BX564047 Glossina morsitans moritans adult infected gut Glossina morsitans moritans cDNA clone Tse6d04_p1c. mRNA sequence.		
ACCESSION	BX564047		
VERSION	BX564047.1		
KEYWORDS	GI:33431246		
SOURCE	EST.		
ORGANISM	Glossina morsitans moritans		
REFERENCE	Glossina morsitans moritans		
AUTHORS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.		
TITLE	1 (bases 1 to 32)		
JOURNAL	Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.		
MEDLINE	Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans moritans and expression analysis of putative immune response genes		
PUBMED	Genome Biol. 4 (10), R63 (2003)		
COMMENT	22881942 14519198 Contact: Hall N Pathogen Sequencing Unit The Sanger Institute The Wellcome Trust Genome Campus Hinxton, Cambridge, CB9 1SA, UK Request for clones, please contact: Mike Lehane Prof. M.J. Lehane School of Biological Sciences, University of Wales, Bangor LL57 2UW All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.		
FEATURES	Location/Qualifiers		
source	1..32 /organism="Glossina morsitans moritans" /mol_type="mRNA" /sub_species="morsitans" /db_xref="taxon:37546" /clones="Tse6d04_p1c" /tissue_type="adult infected gut" /clone_lib="Glossina morsitans moritans adult infected gut" /note="country: Zimbabwe; EST from adult gut infected with T.brucei"		
Query Match	0.3%	Score 21.2;	DB 1; Length 32;
Best Local Similarity	88.5%;	Pred. No. 3.46+02;	
Matches 23;	Conservative 0;	Mismatches 3;	Indels 0; Gaps 0;
QY	4458	ATGGACTTTTTTTTTTTTTTTTTTTT	4483
Db	7	ATAGTTTTTTTTTTTTTTTTTTTTTT	32
RESULT 243			
AZ326012/c			
LOCUS	32 bp	DNA	linear GSS 29-SEP-2000
DEFINITION	1M0048A19R Mouse 10kb plasmid UGCLM library Mus musculus genomic clone UGCLM0048A19 R, genomic survey sequence.		
ACCESSION	AZ326012		
VERSION	AZ326012.1		
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 32)		
TITLE	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.		
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts		

of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

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1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABP-07-G07"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
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Query Match      0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTITTTTTTTTTTTTTTTG 4484
|||||
Db 1 TTTTITTTTTTTTTTTTTTTG 21
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RESULT 245
CF318152      21 bp mRNA linear EST 15-AUG-2003
LOCUS HD--08-C11.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--08-C11, mRNA sequence.
ACCESSION CF318152
VERSION CF318152.1 GI:33689913
KEYWORDS EST.
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SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 21)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
```

```
TITLE Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
JOURNAL of Bioscience and Bioinformatics, Myongji University
COMMENT Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
```

## FEATURES

source

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1. .21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--08-C11"
/tissue_type="callus"
/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
```

line."

```
Query Match      0.3%; Score 21; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4463 CTTTITTTTTTTTTTTTTTTT 4483
|||||
Db 1 CTTTITTTTTTTTTTTTTTTT 21
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RESULT 246
A2792613      21 bp DNA linear GSS 16-FEB-2001
LOCUS 2M045M12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0045M12 F, genomic survey sequence.
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```
ACCESSION A2792613
VERSION A2792613.1 GI:12936725
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
```

```
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von
```

```
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0045 row: M column: 12
Seq primer: CGTTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 21.
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## FEATURES

source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0045M12"
/sex="Male"
/lab_hosts="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```



[illegible]

RESULT 250					
BH000233/c					
LOCUS	BH000233	22 bp	DNA	linear	GSS 27-APR-2001
DEFINITION	2M02871L21R	Mouse 10kb	plasmid	UUGC2M library	Mus musculus genomic
				clone	UUGC2M02871L21 R, genomic survey sequence.

ACCESSION	BH000233
VERSION	BH000233.1
KEYWORDS	GI:13871459
GSS.	
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 22)

**AUTHORS**

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

**JOURNAL** Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: [duunn@genetics.utah.edu](mailto:duunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0287 row: L column: 21  
 Seq primer: CACACAGGAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 22.

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0287L21"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

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Query Match      0.3%; Score 21; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      4463 CTTTTTTTTTTTTTTTTTTT 4483
Db      21 CTTTTTTTTTTTTTTTTTTT 1

RESULT 251
LOCUS   AZ315640/c
DEFINITION AZ315640 23 bp DNA linear GSS 29-SEP-2000
            IM0033004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0033004 F, genomic survey sequence.
ACCESSION AZ315640
VERSION   AZ315640.1 GI:10362861
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0033 row: 0 column: 04
          Seq primer: CGTTGTAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 23.
FEATURES
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            1..23
              Location/Qualifiers
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0033004"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 (gil4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
          Query Match 0.3%; Score 21; DB 1; Length 23;
          Best Local Similarity 100.0%; Pred. No. 1.7e+02;
          Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AZ315640 23 bp DNA linear GSS 29-SEP-2000
LOCUS   IM0033004F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0033004 F, genomic survey sequence.
ACCESSION AZ315640
VERSION   AZ315640.1 GI:10362861
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 23)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0033 row: 0 column: 04
          Seq primer: CGTTGTAACGACGGCCAGT
          Class: plasmid ends
          High quality sequence stop: 23.
FEATURES
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            1..23
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0033004"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
                musculus C57BL/6J (male) was obtained from the Jackson
                Laboratory Mouse DNA Resource
                (http://www.jax.org/resources/documents/dnares/). The DNA
                was hydrodynamically sheared by repeated passage through a
                0.005 inch orifice at constant velocity. The sheared DNA
                was blunt end-repaired with T4 DNA polymerase and T4
                polynucleotide kinase. Adaptor oligonucleotides were
                ligated to the blunt ends in high molar excess. The
                adapted DNA was purified and size-selected for a 9.5 to
                10.5 kb range using preparative agarose gel
                electrophoresis. Vector DNA was prepared from a derivative
                of PWD42 (gil4732114|gb|AF129072.1), a copy-number
                inducible derivative of plasmid R1. The vector was ligated
                with adaptors complementary to the insert adaptors and
                purified. The sheared, adapted mouse DNA was annealed to
                adapted vector DNA, and transformed into
                chemically-competent E. coli XL10-Gold (Stratagene) cells
                and selected for ampicillin resistance."
          Query Match 0.3%; Score 21; DB 1; Length 23;
          Best Local Similarity 100.0%; Pred. No. 1.7e+02;
          Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4464 TTTTTTTTTTTTTTTTTTTT 4484
Db      23 TTTTTTTTTTTTTTTTTTTT 3

RESULT 252
LOCUS   CF326993/c
DEFINITION CF326993 24 bp mRNA linear EST 18-AUG-2003
            NACL--01-E17.g1 Rice callus plasmid cDNA library (NACL) Oryza
            sativa cDNA clone NACL--01-E17, mRNA sequence.
ACCESSION CF326993
VERSION   CF326993.1 GI:33802241
KEYWORDS EST.
SOURCE   Oryza sativa
ORGANISM Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 24)
AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.
FEATURES
          source
            1..24
              Location/Qualifiers
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="NACL--01-E17"
                /tissue_type="callus"
                /dev_stage="proliferated callus on 2N6 media for 30 days"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice callus plasmid cDNA library (NACL)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."
          Query Match 0.3%; Score 21; DB 1; Length 24;
          Best Local Similarity 100.0%; Pred. No. 1.9e+02;
          Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTTTTTTTTTTTTTTTTTT 4484
Db      22 TTTTTTTTTTTTTTTTTTTT 2

RESULT 253
LOCUS   AZ404871/c
DEFINITION AZ404871 24 bp DNA linear GSS 03-OCT-2000
            IM0173J14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0173J14 R, genomic survey sequence.
ACCESSION AZ404871
VERSION   AZ404871.1 GI:10528884
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
          Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
          Query Match 0.3%; Score 21; DB 1; Length 24;
          Best Local Similarity 100.0%; Pred. No. 1.9e+02;
          Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



Generation and analysis of 280,000 human expressed sequence tags	
Genome Res. 6 (9), 807-828 (1996)	
97044478	
PUBMED	
COMMENT	
Contact: Wilson RK	
Washington University School of Medicine	
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108	
Tel: 314 286 1800	
Fax: 314 286 1810	
Email: est@watson.wustl.edu	
High quality sequence starts: 1	
High quality sequence stops: 1	
Source: IMAGE Consortium, LLNL	
This clone is available royalty-free through LLNL; contact the	
IMAGE Consortium (info@image.llnl.gov) for further information.	
Trace considered overall poor quality	
Seq primer: ml3 -40 forward	
High quality sequence stop: 1.	
Location/Qualifiers	
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/organism="Homo sapiens"	
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/db_xref="taxon:9606"	
/clone="IMAGE:255706"	
/sex="Female"	
/tissue_type="olfactory epithelium"	
/dev_stage="35 year old"	
/lab_host="SOLR cells (kanamycin resistant)"	
/clone_lib="Weizmann Olfactory Epithelium"	
/notes="Organ: nose; Vector: pBluescript SK-; Site_1:	
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:	
Oligo dT. Olfactory epithelium, normal. Average insert	
size: 0.8 kb; Uni-ZAP XR Vector. Library constructed by N.	
Walker, D. Lancet, Weizmann Institute of Science. -5'	
adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor	
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'	
Query Match 0.3%; Score 21; DB 1; Length 25;	
Best Local Similarity 100.0%; Pred. No. 2.1e+02;	
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT G 4484	
Db 2 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT G 22	
RESULT 256	
CG726337	
LOCUS	
DEFINITION	
1119089E312.2ELy1 1119 - RescueMu Grid AA Zea mays genomic, genomic	
survey sequence.	
CG726337	
CG726337.1 GI:37764992	
KEYWORDS	
SOURCE	
ORGANISM	
Zea mays	
Zea mays	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD	
clade; Panicoideae; Andropogoneae; Zea.	
1 (bases 1 to 25)	
Walbot, V.	
Maize genomic sequences found using engineered RescueMu transposon	
Unpublished (2001)	
Contact: Walbot V	
Department of Biological Sciences	
Stanford University	
855 California Ave, Palo Alto, CA 94304, USA	
Tel: 650 723 2227	
Fax: 650 725 8221	
Email: walbot@stanford.edu	
Possible ligation site of ends cut by 2 different endonucleases.	
Reverse complemented post-ligation sequence from source sequence.	







**TITLE**  
JOURNAL

**COMMENT**  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org

**FEATURES**  
source  
Location/Qualifiers  
1..30

/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strain="TREU927"  
/db\_xref="taxon:5691"  
/clone="226905"

**Query Match**  
Best Local Similarity 0.3%; Score 21; DB 1; Length 30;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**QY** 4455 GGCATGGACTTTTTTTTTTTTTTTTTTTTTTTT 4483  
|||||  
**DB** 29 GGGGGGGGGTTTTTTTTTTTTTTTTTTTTTTT 1

**RESULT 264**  
**CF311684**  
**LOCUS**  
**DEFINITION** ABF--07-A15-g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--07-A15, mRNA sequence.  
**ACCESSION** CF311684  
**VERSION** CF311684.1 GI:33683445  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Oryza sativa  
**REFERENCE** 1 (bases 1 to 31)  
**AUTHORS** Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

**FEATURES**  
source  
Location/Qualifiers  
1..31

/organism="Oryza sativa"  
/mol\_type="mRNA"  
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/db\_xref="taxon:4530"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/note="vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and

then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

**Query Match**  
Best Local Similarity 0.3%; Score 21; DB 1; Length 31;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**QY** 4455 GGCATGGACTTTTTTTTTTTTTTTTTTTTTTTT 4483  
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**DB** 1 GGCATGACAGTGTGTGTGTGTGTGTGTGT 29

**RESULT 265**  
**CF312635**  
**LOCUS**  
**DEFINITION** ABF--08-H15-g1 ABF3-overexpressing transgenic rice plasmid cDNA library (ABF) Oryza sativa cDNA clone ABF--08-H15, mRNA sequence.  
**ACCESSION** CF312635  
**VERSION** CF312635.1 GI:33684396  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Oryza sativa  
**REFERENCE** 1 (bases 1 to 31)  
**AUTHORS** Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
**TITLE** Large-scale Sequencing Analysis of Rice ESTs  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

**FEATURES**  
source  
Location/Qualifiers  
1..31

/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
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/lab\_host="E.coli DH10B"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
/note="vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

**Query Match**  
Best Local Similarity 0.3%; Score 21; DB 1; Length 31;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

**QY** 4455 GGCATGGACTTTTTTTTTTTTTTTTTTTTTTTT 4483  
|||||  
**DB** 2 GGCATGACAGTGTGTGTGTGTGTGTGT 30

**RESULT 266**  
**AV675687**  
**LOCUS**  
**DEFINITION** AV675687 Nori Satoh unpublished cDNA library Ciona intestinalis cDNA clone citb13c7 5', mRNA sequence.  
**ACCESSION** AV675687  
**VERSION** AV675687.1 GI:10113686  
**KEYWORDS** EST.



Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1..32  
/organism="Glossina morsitans morsitans"  
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/db\_xref="taxon:37546"  
/clone="Tse21g09\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.3%; Score 21; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTGTGTGTGTGTGTGTGTGTGTGTGT 4484  
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Db 12 TTTTGTGTGTGTGTGTGTGTGTGTGTGT 32  
|||||

RESULT 270  
BX555625  
LOCUS  
DEFINITION BX555625 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse21g09\_plc, mRNA sequence.  
ACCESSION BX555625  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehan  
Prof. M.J. Lehan  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1..32  
/organism="Glossina morsitans morsitans"  
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/clone="Tse21g09\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.3%; Score 21; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTGTGTGTGTGTGTGTGTGTGTGTGT 4484  
|||||  
Db 12 TTTTGTGTGTGTGTGTGTGTGTGTGTGT 32  
|||||

RESULT 270  
BX555625  
LOCUS  
DEFINITION BX555625 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse21g09\_plc, mRNA sequence.  
ACCESSION BX555625  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehan  
Prof. M.J. Lehan  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1..32  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse21g09\_plc"  
/tissue\_type="adult infected gut"  
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gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.3%; Score 21; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4465 TTTTGTGTGTGTGTGTGTGTGTGTGTGT 4485  
|||||  
Db 11 TTTTGTGTGTGTGTGTGTGTGTGTGTGT 31  
|||||

RESULT 272  
BG670391/c  
LOCUS  
DEFINITION BG670391 Rat DRG Library Rattus norvegicus cDNA clone DRNBAF06 5',  
mRNA sequence.

/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.3%; Score 21; DB 1; Length 32;  
Best Local Similarity 82.8%; Pred. No. 3.7e+02;  
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTGTGTGTGTGTGTGTGTGTGTGTGT 4487  
|||||  
Db 4 TAGATAGTTTGTGTGTGTGTGTGTGTGTGTGTGT 32  
|||||

RESULT 271  
BX557354  
LOCUS  
DEFINITION BX557354 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse31g07\_plc, mRNA sequence.  
ACCESSION BX557354  
VERSION  
KEYWORDS  
SOURCE EST.  
ORGANISM Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 32)  
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehan  
Prof. M.J. Lehan  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

FEATURES  
source  
Location/Qualifiers  
1..32  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse31g07\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.3%; Score 21; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4465 TTTTGTGTGTGTGTGTGTGTGTGTGTGT 4485  
|||||  
Db 11 TTTTGTGTGTGTGTGTGTGTGTGTGTGT 31  
|||||

RESULT 272  
BG670391/c  
LOCUS  
DEFINITION BG670391 Rat DRG Library Rattus norvegicus cDNA clone DRNBAF06 5',  
mRNA sequence.



/clone lib="cdna Peking library 12hr SCN3"  
/note="Vector: pBluescript SK-; cDNA clones from mRNA  
extracted from roots of soybean cv. Peking 12 hrs after  
infection by SCN race 3. These are cloned in pBluescript  
SK- phagemid."

Query Match 0.3%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 2e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4460 GCACATTTTTTTTTTTTTTTTTTTT 4483  
Db 1 GGTATTTTTTTTTTTTTTTTTTTT 24

RESULT 275  
CF276855/c  
LOCUS  
DEFINITION  
Oryza sativa cDNA clone 14ETL--02-C19, mRNA sequence.  
ACCESSION  
CF276855  
VERSION  
CF276855.1 GI:33654241  
KEYWORDS  
EST.  
SOURCE  
Oryza sativa

ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE  
1 (bases 1 to 24)  
AUTHORS  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
TITLE  
Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL  
Unpublished (2003)  
COMMENT  
Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
source  
1..24  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ETL--02-C19"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice etiolated leaf plasmid cDNA library  
(14ETL)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 2e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTITTTTTTTTTTTTTTTTGTCT 4487  
Db 24 TTTTITTTTTTTTTTTTTTTT 1

RESULT 276  
CF301561  
LOCUS  
DEFINITION  
7LEAF--06-H15, b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--06-H15, mRNA sequence.  
ACCESSION  
CF301561  
VERSION  
CF301561.1 GI:33673322  
KEYWORDS  
EST.

SOURCE  
ORGANISM

Oryza sativa  
Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
source

1..24  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--06-H15"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site\_1: EcoRI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.3%; Score 20.8; DB 1; Length 24;  
Best Local Similarity 91.7%; Pred. No. 2e+02;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTITTTTTTTTTTTTTTTTGTCT 4487  
Db 1 TTTTITTTTTTTTTTTTTTTT 24

RESULT 277  
CF312319  
LOCUS

DEFINITION

ABF--07-P12, g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--07-P12, mRNA sequence.

ACCESSION

CF312319

VERSION

CF312319.1 GI:33684080

KEYWORDS

EST.

SOURCE

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaeae; Oryza.

REFERENCE

AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE

Large-scale Sequencing Analysis of Rice ESTs

JOURNAL

Unpublished (2003)

COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES

source

1..24  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="ABF--07-P12"

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/tissue type="leaf"
/dev stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4460 GGACTTTTTTTTTTTTTTTTTTTT 4487
||| ||||| ||||| ||||| ||||| |||||
Db 1 GGT|TTTTTTTTTTTTTTTTTTTTTTT 24

RESULT 278
CF320862
LOCUS      24 bp mRNA linear EST 15-AUG-2003
DEFINITION HD--11-O12.b1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa cDNA clone HD--11-O12, mRNA sequence.
ACCESSION  CF320862
VERSION     CF320862.1 GI:33692623
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..24
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--11-O12"
/tissue type="callus"
/dev stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli DH10B"
/clone_lib="OSHDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT|TTTTTTTTTTTTTTTTTGTCT 4487
||| ||||| ||||| ||||| ||||| |||||
Db 1 TTTT|TTTTTTTTTTTTTTTTTGTCT 24

RESULT 279
CF320862
LOCUS      24 bp DNA linear GSS 29-SEP-2000
DEFINITION Clone UUGC1M0052M17 R, genomic survey sequence.
ACCESSION  AZ328848
VERSION     AZ328848.1 GI:10388979
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 24)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,W., Rose,M., Rose,R., Stokes,R., fingeay,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: M column: 17
Seq primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0052M17"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (G|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 20.8; DB 1; Length 24;
Best Local Similarity 91.7%; Pred. No. 2e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTT|TTTTTTTTTTTTTTTTTGTCT 4487
||| ||||| ||||| ||||| ||||| |||||
Db 24 TTTT|TTTTTTTTTTTTTTTTTGTCT 1

RESULT 280
AZ363562/c

```





<hr/>					
clone UUGC1M0152H07 F, genomic survey sequence.					
ACCESSION	AZ390642				
VERSION	AZ390642.1	GI:10505685			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0152 row: H column: 07 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 24.				
FEATURES	source				
	1..24				
	/organism="Mus musculus"				
	/mol_type="genomic DNA"				
	/strain="C57BL/6J"				
	/db_xref="taxon:10090"				
	/clone="UUGC1M0152H07"				
	/sex="Male"				
	/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"				
	/clone_lib="Mouse 10kb plasmid UUC1M library"				
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
	Query Match 0.3%; Score 20.8; DB 1; Length 24;				
	Best Local Similarity 91.7%; Pred. No. 2e+02;				
	Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	4464	TTTTTTTTTTTTTTTTTTTGCT	4487		
Db	1	TTTTTTTTTTTTTTTTTTTTTTT	24		
RESULT 283					
AZ459280					
LOCUS	AZ459280	24 bp	DNA	linear	GSS 04-OCT-2000
DEFINITION	IM0264A05F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUGC1M0264A05 F, genomic survey sequence.				
ACCESSION	AZ459280				
VERSION	AZ459280.1	GI:10617405			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunne@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0152 row: H column: 07 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 24.				
FEATURES	source				
	1..24				
	/organism="Mus musculus"				
	/mol_type="genomic DNA"				
	/strain="C57BL/6J"				
	/db_xref="taxon:10090"				
	/clone="UUGC1M0152H07"				
	/sex="Male"				
	/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"				
	/clone_lib="Mouse 10kb plasmid UUC1M library"				
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."				
	Query Match 0.3%; Score 20.8; DB 1; Length 24;				
	Best Local Similarity 91.7%; Pred. No. 2e+02;				
	Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;				
Qy	4464	TTTTTTTTTTTTTTTTTTTGCT	4487		
Db	1	TTTTTTTTTTTTTTTTTTTTTTT	24		
RESULT 284					
AZ644621					
LOCUS	AZ644621	24 bp	DNA	linear	GSS 14-DEC-2000
DEFINITION	IM0508F12R Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUGC1M0508F12 R, genomic survey sequence.				
ACCESSION	AZ644621				
VERSION	AZ644621.1	GI:10617405			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				









RECESSION  
VERSION  
KEYWORDS







```
ACCESSION AL483278
VERSION AL483278.1 GI:11849602
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 27)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T\_brucei/.
FEATURES
source
1..27
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="257b07"
Query Match 0.3%; Score 20.8; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 2.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4464 TTTTNTTTTTTTTTTTTTTTTGCTT 4488
Db 27 TTTTNTTTTTTTTTTTTTTTT 3
RESULT 302
AU257468
LOCUS AU257468 28 bp mRNA linear EST 25-APR-2002
DEFINITION AU257468 3'-directed mouse cDNA library Mus musculus cDNA clone
BED0010669 3', mRNA sequence.
ACCESSION AU257468
VERSION AU257468.1 GI:20322117
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 28)
AUTHORS Kato,K. and Matoba,R.
TITLE Generation of expressed sequence tags from mouse brain
JOURNAL Unpublished (2002)
COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kkatob@s.aist-nara.ac.jp,
URL: http://love2.aist-nara.ac.jp/BED/index.html.
Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="BED0010669"
/tissue_type="brain"
/clone_lib="3'-directed mouse cDNA library"
Query Match 0.3%; Score 20.8; DB 1; Length 28;
Best Local Similarity 88.0%; Pred. No. 2.9e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4463 CTTTNTTTTTTTTTTTTTTTTGCTT 4487
Db 4 CTTTNTTTTTTTTTTTTTTTT 28
RESULT 303
CF277114
LOCUS CF277114 28 bp mRNA linear EST 14-AUG-2003
DEFINITION 14ETL--02-111.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--02-111, mRNA sequence.
ACCESSION CF277114
VERSION CF277114.1 GI:33654500
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 28)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..28
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--02-111"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/note="Vector: pCR4-TOPO; Site:1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.3%; Score 20.8; DB 1; Length 28;
Best Local Similarity 91.1%; Pred. No. 2.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 4464 TTTTNTTTTTTTTTTTTTTTTGCTT 4487
Db 2 TTTTNTTTTTTTTTTTTGT 25
RESULT 304
CF299294/c
LOCUS CF299294 28 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--03-E04.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--03-E04, mRNA sequence.
ACCESSION CF299294
VERSION CF299294.1 GI:33671055
KEYWORDS EST.
SOURCE Oryza sativa
```

```

ORGANISM      Oryza sativa
REFERENCE      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Ehrhartoideae; Oryzeae; Oryza.
                1 (bases 1 to 28)
                Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
                Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT        Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 321 6193
                Fax: 82 31 321 6355
                Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES      Location/Qualifiers
                source
                1..28
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="7LEAF-03-E04"
                /tissue_type="leaf"
                /dev_stages="7 days after germination"
                /lab_host="E.coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.3%; Score 20.8; DB 1; Length 28;
Best Local Similarity 91.7%; Pred. No. 2.9e+02;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      4464 TTTTTCCTTTTTCCTTTTTCCTTCCT 4487
Db      24 TTTTTCCTTTTTCCTTTTTCCTTCCT 1

RESULT 305
T56352
LOCUS          T56352      28 bp      mRNA      linear      EST 06-FEB-1995
DEFINITION    YB34C09.g1 Stratagene fetal spleen (#937205) Homo sapiens cDNA
                clone IMAGE:73072 3' similar to gb:S41458 ROD
                CGMP-SPECIFIC 3', 5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT (HUMAN),
                mRNA sequence.
ACCESSION     T56352      1 GI:658213
VERSION       T56352.1
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens

REFERENCE      Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                1 (bases 1 to 28)
                Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
                Chisoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
                Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
                Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
                Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,P., Thierry-Mieg,J.,
                Trevaaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                and Marra,M.
TITLE          Generation and analysis of 280,000 human expressed sequence tags
JOURNAL        Genome Res. 6 (9), 807-828 (1996)
MEDLINE       97044478
PUBMED        8889549
COMMENT        Contact: Wilson RK
                Washington University School of Medicine
                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                Tel: 314 286 1800
                Fax: 314 286 1810
                Email: est@watson.wustl.edu
                High quality sequence starts: 1

Oryza sativa
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Seq primer: -21ml3
High quality sequence stop: 1.
Location/Qualifiers
                1..28
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="GDB:494737"
                /db_xref="taxon:9606"
                /clone="IMAGE:73072"
                /tissue_type="fetal spleen"
                /dev_stages="fetal"
                /lab_host="SOLR cells (kanamycin resistant)"
                /clone_lib="Stratagene fetal spleen (#937205)"
                /note="Organ: spleen; Vector: pBluescript SK-; Site 1:
                EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
                Oligo dT. Pooled spleens. Average insert size: 1.0 kb;
                Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGACGAG
                3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."

Query Match      0.3%; Score 20.8; DB 1; Length 28;
Best Local Similarity 88.0%; Pred. No. 2.9e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      4459 TGGACTTTTTCCTTTTTCCTTTTTCCTTCCT 4483
Db      3 TTNATTTTTCCTTTTTCCTTTTTCCTTCCT 27

RESULT 306
BX568640
LOCUS          BX568640      29 bp      mRNA      linear      EST 14-OCT-2003
DEFINITION    morsitans morsitans cDNA clone Tse95a01_plc, mRNA sequence.
ACCESSION     BX568640
VERSION       BX568640.1 GI:33435499
KEYWORDS      EST.
SOURCE        Glossina morsitans morsitans
ORGANISM      Glossina morsitans morsitans
                Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Hippoboscidae; Glossinidae; Glossina.
                1 (bases 1 to 29)
                Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
                Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
                Adult midgut expressed sequence tags from the tsetse fly Glossina
                morsitans morsitans and expression analysis of putative immune
                response genes
JOURNAL        Genome Biol. 4 (10), R63 (2003)
MEDLINE       22881942
PUBMED        14519198
COMMENT        Contact: Hall N
                Pathogen Sequencing Unit
                The Sanger Institute The Wellcome Trust Genome Campus
                Hinxton, Cambridge, CB10 1SA, UK
                Request for clones, please contact: Mike Lehane
                Prof. M.J. Lehane
                School of Biological Sciences,
                University of Wales,
                Bangor LL57 2UW
                All clones with suffix qic are reverse primer reads starting at 5'
                end of the cDNA all pic reads are from
                the 3' end.

FEATURES      Location/Qualifiers
                source
                1..29
                /organism="Glossina morsitans morsitans"
                /mol_type="mRNA"
                /sub_species="morsitans"
                /db_xref="taxon:37546"

```



	Best Local Similarity	91.7%;	Pred. No.	3.7e+02;
	Matches	22; Conservative	0; Mismatches	2; Indels
			Gaps	0;
Qy	5270	CCATAGGGACGAGTGTGCAGCCTC	5293	
Dd	29	CCATAGGAAGTAGTGCGAGCCTC	6	

```

RES011_311
AV958999
LOCUS
DEFINITION
  AV958999 Nori Satoh unpublished cDNA library, young adult Ciona
  intestinalis cDNA clone ciad11922 5', mRNA sequence.
ACCESSION
  AV958999
VERSION
  AV958999.1 GI:19447298
KEYWORDS
  EST.
SOURCE
  Ciona intestinalis
  Ciona intestinalis
  Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
  Phlebobranchia; Clonidae; Ciona.
REFERENCE
  Satoh,N., Satou,Y., Kohara,Y. and Shin-i.T.
  Expressed genes in Ciona intestinalis
  Unpublished (2000)
  Contact: Nori Satoh
  Department of Zoology
  Kyoto University
  Sakyo-ku, Kyoto 606-8502, Japan
  Tel: 81-75-753-4081
  Fax: 81-75-705-1113
  Email: sath@ascidian.zool.kyoto-u.ac.jp.
  Location/Qualifiers
    1..32
      /organism="Ciona intestinalis"
      /mol_type="mRNA"
      /db_xref="taxon:7719"
      /clone="ciad11922"
      /tissue_type="whole animal"
      /dev_stage="young adult"
      /clone_lib="Nori Satoh unpublished cDNA library, young
      adult"
FEATURES
  source

```

Query Match	0.3%;	Score 20.8;	DB 1;	Length 32;
Best Local Similarity	78.1%;	Pred. No. 4e+02;		
Matches 25;	Conservative 0;	Mismatches 7;	Indels 0;	Gaps 0;
QY	4449	GTGGGTGGCATGCAC	TTTTTTTTTTTTTTTTTTTT	4480
DB	1	GAGGCTAGTCTCGAGT	TTTTTTTTTTTTTTTTTTTT	32
RESULT 312				
CF296152/c				
LOCUS				
DEFINITION	30DGS--06-G09 b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--06-G09, mRNA sequence.	32 bp mRNA linear	EST 14-AUG-2003	
ACCESSION	CF296152			
VERSION	CF296152.1	GI:33665185		
KEYWORDS	EST.			
SOURCE	Oryza sativa			
ORGANISM	Oryza sativa			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoideae; Oryza.			
REFERENCE	1	(bases 1 to 32)		
AUTHORS	Kim, J. S., Jun, K. M., Cheong, P. J., Kim, M. J., Lee, T. H., Shin, Y. C., Song, S. I., Kim, J. K., Kim, Y. -K. and Nahm, B. H.			
TITLE	Large-scale Sequencing Analysis of Rice ESTs			
JOURNAL	Unpublished (2003)			
COMMENT	Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Gyeonggi, Korea			

0.3%; Score 20.8; DB 1; Length 31;

Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

#### FEATURES source

```

1. .32
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--06-G09"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Pice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TORO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

Query Match 0.3%; Score 20.8; DB 1; Length 32;  
 Best Local Similarity 78.1%; Pred. No. 4e+02;  
 Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4020 AAAAAAGAGAGAAACAAAATGTTATTTTAT 4051  
 ||||| | | | | | | | | | | | | | | | |  
 Db 32 AAAAAAAAAAAAAAAAAATTTTTTTTTT 1

#### RESULT 313

AZ345558  
 LOCUS  
 DEFINITION AZ345558 32 bp DNA linear GSS 29-SEP-2000  
 clone UGCLM0080G16 F, genomic survey sequence.  
 ACCESSION AZ345558  
 VERSION AZ345558.1 GI:10424795  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 32)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Isalam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausen,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0080 row: G column: 16  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 32.

#### FEATURES source

```

1. .32
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCLM0080G16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UGCLM library"
/notes="Vector: PMD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource

```

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20.8; DB 1; Length 32;  
 Best Local Similarity 78.1%; Pred. No. 4e+02;  
 Matches 25; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 5317 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 5348  
 ||||| | | | | | | | | | | | | | | | |  
 Db 1 TCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 32

#### RESULT 314

CG707472  
 LOCUS  
 DEFINITION CG707472 32 bp DNA linear GSS 20-OCT-2003  
 survey sequence.  
 ACCESSION CG707472  
 VERSION CG707472.1 GI:37733378  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 32)  
 Walbot,V.  
 Maize genomic sequences found using engineered RescueMu transposon  
 Unpublished (2001)  
 Contact: Walbot V  
 Department of Biological Sciences  
 Stanford University  
 855 California Ave, Palo Alto, CA 94304, USA  
 Tel: 650 723 2227  
 Fax: 650 725 8221  
 Email: walbot@stanford.edu  
 Possible ligation site of ends cut by 2 different endonucleases.  
 Reverse complemented post-ligation sequence from source sequence.  
 Plate: 119002 row: F column: 02  
 Class: transposon-tagged.  
 Location/Qualifiers  
 1. .32  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultivar="mixed background W23/A188/B73/K55"  
 /db\_xref="taxon:4577"  
 /tissue\_type="leaf"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="1119 - RescueMu Grid AA"  
 /notes="Organ: leaf; Vector: RescueMu (engineered from  
 pBluescript backbone); Site 1: BamHI; Site 2: BglII;  
 RescueMu is a 4.9 kb, modified maize Mu transposon  
 designed to allow plasmid rescue from total genomic DNA.  
 Mu elements insert preferentially into transcription  
 units. For more information on RescueMu, go to the web  
 site 'www.zmdb.iastate.edu' and follow the links for  
 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA  
 was extracted from leaf strips, double digested using

#### FEATURES source

```

1. .32
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - RescueMu Grid AA"
/notes="Organ: leaf; Vector: RescueMu (engineered from
pBluescript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site 'www.zmdb.iastate.edu' and follow the links for
'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using

```



```

/dev stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH108"
/clone_lib="rice callus plasmid cDNA library (NACL)"
/notes="vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

```

Query Match      0.3%; Score 20.6; DB 1; Length 29;
Best Local Similarity 85.2%; Pred. No. 3.4e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```
QY 4464 TTTTCTTTTCTTTTCTTTTCTTTGCTCTGA 4490
```

```
Db 1 TTTTCTTTTCTTTTCTTTTCTTTTGGAGTGA 27
```

```

RESULT 318
BX553986
LOCUS      30 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse131902_plc, mRNA sequence.
ACCESSION  BX553986
VERSION     BX553986.1 GI:33378096
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Glossina morsitans morsitans

```

```

REFERENCE  1 (bases 1 to 30)
AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
          Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
          morsitans morsitans and expression analysis of putative immune
          response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PubMed   14519198
COMMENT   Contact: Hall N
          The Sanger Institute The Wellcome Trust Genome Campus
          Hinxton, Cambridge, CB10 1SA, UK
          Request for clones, please contact: Mike Lehane
          Prof. M.J.Lehane
          School of Biological Sciences,
          University of Wales,
          Bangor LL57 2UW
          All clones with suffix g1c are reverse primer reads starting at 5'
          end of the cDNA all plc reads are from
          the 3' end.

```

```

FEATURES             source
    source
1..30
/mol_type="mRNA"
/organism="Glossina morsitans morsitans"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse131902_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.3%; Score 20.6; DB 1; Length 30;
Best Local Similarity 85.2%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```
QY 4459 TGGACTTTTCTTTTCTTTTCTTTTCTTTTGT 4485
```

```
Db 4 TAGATAGTTTCTTTTCTTTTCTTTTCTTTTGT 30
```

```

RESULT 320
BX554615
LOCUS      31 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse16d08_plc, mRNA sequence.
ACCESSION  BX554615
VERSION     BX554615.1 GI:33378687
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Glossina morsitans morsitans

```

```

REFERENCE  1 (bases 1 to 31)
AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
          Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
          morsitans morsitans and expression analysis of putative immune
          response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PubMed   14519198
COMMENT   Contact: Hall N
          The Sanger Institute The Wellcome Trust Genome Campus
          Hinxton, Cambridge, CB10 1SA, UK
          Request for clones, please contact: Mike Lehane
          Prof. M.J.Lehane
          School of Biological Sciences,
          University of Wales,
          Bangor LL57 2UW
          All clones with suffix g1c are reverse primer reads starting at 5'
          end of the cDNA all plc reads are from
          the 3' end.

```

```
QY 4459 TGGACTTTTCTTTTCTTTTCTTTTCTTTTGT 4485
```

```
Db 4 TAGATAGTTTCTTTTCTTTTCTTTTCTTTTGT 30
```

```
RESULT 319
```

```

BX554037
LOCUS      30 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse13a07_plc, mRNA sequence.
ACCESSION  BX554037
VERSION     BX554037.1 GI:33378144
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Glossina morsitans morsitans

```

```

REFERENCE  1 (bases 1 to 30)
AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
          Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
          morsitans morsitans and expression analysis of putative immune
          response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PubMed   14519198
COMMENT   Contact: Hall N
          The Sanger Institute The Wellcome Trust Genome Campus
          Hinxton, Cambridge, CB10 1SA, UK
          Request for clones, please contact: Mike Lehane
          Prof. M.J.Lehane
          School of Biological Sciences,
          University of Wales,
          Bangor LL57 2UW
          All clones with suffix g1c are reverse primer reads starting at 5'
          end of the cDNA all plc reads are from
          the 3' end.

```

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FEATURES             source
    source
1..30
/mol_type="mRNA"
/organism="Glossina morsitans morsitans"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse13a07_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.3%; Score 20.6; DB 1; Length 30;
Best Local Similarity 85.2%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

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QY 4459 TGGACTTTTCTTTTCTTTTCTTTTCTTTTGT 4485
```

```
Db 4 TAGATAGTTTCTTTTCTTTTCTTTTCTTTTGT 30
```

```

RESULT 320
BX554615
LOCUS      31 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse16d08_plc, mRNA sequence.
ACCESSION  BX554615
VERSION     BX554615.1 GI:33378687
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Glossina morsitans morsitans

```

```

REFERENCE  1 (bases 1 to 31)
AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
          Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
          morsitans morsitans and expression analysis of putative immune
          response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PubMed   14519198
COMMENT   Contact: Hall N
          The Sanger Institute The Wellcome Trust Genome Campus
          Hinxton, Cambridge, CB10 1SA, UK
          Request for clones, please contact: Mike Lehane
          Prof. M.J.Lehane
          School of Biological Sciences,
          University of Wales,
          Bangor LL57 2UW
          All clones with suffix g1c are reverse primer reads starting at 5'
          end of the cDNA all plc reads are from
          the 3' end.

```

```

FEATURES             source
    source
1..30
/mol_type="mRNA"
/organism="Glossina morsitans morsitans"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse13a07_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.3%; Score 20.6; DB 1; Length 30;
Best Local Similarity 85.2%; Pred. No. 3.7e+02;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```





```

VERSION      AW323399.1  GI:6828756
KEYWORDS
SOURCE       Pneumocystis carinii
ORGANISM     Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;
              Pneumocystidaceae; Pneumocystis.
REFERENCE    1 (bases 1 to 22)
AUTHORS      Smullan,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,
              Edman,J.C., Kovacs,J. and Cushion,M.
TITLE        Expressed sequence tags from Pneumocystis carinii
JOURNAL      Unpublished (2000)
COMMENT      Contact: Staben C
              School of Biological Sciences
              University of Kentucky
              101 Morgan Building, University of Kentucky, Lexington, KY
              40506-0225, USA
              Tel: 606 257 2161
              Fax: 606 257 1717
              Email: staben@pop.uky.edu.

FEATURES     source
              1..22
                /organism="Pneumocystis carinii"
                /mol_type="mRNA"
                /db_xref="taxon:4754"
                /lab_host="E. coli"
                /clone_lib="AGS-1"
                /note="vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;
                P. carinii organisms (3x10e9) from a single rat (99-1-6,
                sacrificed on 3/17/99) at Cincinnati VA facilities.
                Trizol extracted RNA. Oligo dt priming, standard
                conditions described by vendor. Stratagene. Further
                details see www.uky.edu/Project/Pneumocystis/"

Query Match      0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4464  TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB      1      TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 324
CF299342
LOCUS       CF299342                22 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--03-F06.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--03-F06, mRNA sequence.
ACCESSION   CF299342
VERSION     CF299342.1  GI:33671103
KEYWORDS    EST.
SOURCE      Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 22)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
              1..22
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="7LEAF--03-F06"
                /tissue_type="leaf"
                /dev_stage="7 days after germination"
                /lab_host="E. coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4464  TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB      1      TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 326
CF310366
LOCUS       CF310366                22 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  ABF--04-P14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
              library (ABF) Oryza sativa cDNA clone ABF--04-P14, mRNA sequence.
ACCESSION   CF310366

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/clone="7LEAF--03-F06"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E. coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4464  TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB      1      TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 325
CF300133
LOCUS       CF300133                22 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--04-G19.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
              sativa cDNA clone 7LEAF--04-G19, mRNA sequence.
ACCESSION   CF300133
VERSION     CF300133.1  GI:33671894
KEYWORDS    EST.
SOURCE      Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
            1 (bases 1 to 22)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES     source
              1..22
                /organism="Oryza sativa"
                /mol_type="mRNA"
                /cultivar="Nackdong"
                /db_xref="taxon:4530"
                /clone="7LEAF--04-G19"
                /tissue_type="leaf"
                /dev_stage="7 days after germination"
                /lab_host="E. coli DH10B"
                /clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
                /note="vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
                with oligoribonucleotides and then used as templates for
                RT-PCR."

Query Match      0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4464  TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
DB      1      TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 326
CF310366
LOCUS       CF310366                22 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  ABF--04-P14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
              library (ABF) Oryza sativa cDNA clone ABF--04-P14, mRNA sequence.
ACCESSION   CF310366

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

```

**KEYWORDS**  
Mus musculus (house mouse)

**SOURCE ORGANISM**  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 22)

**REFERENCE AUTHORS**  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Iglam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

**JOURNAL COMMENT**  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLUC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0127 row: H column: 16  
Seq primer: CGTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

**FEATURES**

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1..22	/organism="Mus musculus"
	/mol_type="genomic DNA"
	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="UUGCIM0127H16"
	/sex="Male"
	/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
	/clone_lib="Mouse 10kb plasmid UUGCIM library"
	/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57Bl/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi 4732114 gb AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**Query Match**  
Best Local Similarity 0.3%; Score 20.4; DB 1; Length 22;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 4465 TTTTTTTTTTTTTTTTTTTTGTC 4486

**Db** 22 TTTTTTTTTTTTTTTTTTTTTC 1

**RESULT 340**  
**AZ388103/c**  
**LOCUS** AZ388103  
**DEFINITION** 1M0147N14R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0147N14 R, genomic survey sequence.  
**ACCESSION** AZ388103  
**VERSION** AZ388103.1 GI:10501811  
**KEYWORDS** GSS.





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REFERENCE
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 22)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0212 row: A column: 05
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 22.
FEATURES     source
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                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0212A05"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              Query Match      0.3%; Score 20.4; DB 1; Length 22;
              Best Local Similarity 95.5%; Pred. No. 1.9e+02;
              Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
          |||||
Db    1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 344
LOCUS    AZ459654
DEFINITION AZ459654 22 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0264G12 R, genomic survey sequence.
ACCESSION AZ459654
VERSION    AZ459654.1 GI:10617779
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
              Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
              Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
              Niederhausern,A. and Wright,D.,Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
              plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
              University of Utah Genome Center
              University of Utah
              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
              84112, USA
              Tel: 801 585 5606
              Fax: 801 585 7177
              Email: ddunn@genetics.utah.edu
              Insert Length: 10000 Std Error: 0.00
              Plate: 0264 row: G column: 12
              Seq primer: CACACAGGAACAGCTATGACC
              Class: plasmid ends
              High quality sequence stop: 22.
FEATURES     source
              1. .22
                /organism="Mus musculus"
                /mol_type="genomic DNA"
                /strain="C57BL/6J"
                /db_xref="taxon:10090"
                /clone="UUGC1M0264G12"
                /sex="Male"
                /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                /clone_lib="Mouse 10kb plasmid UUGC1M library"
                /notes="Vector: PWD42nv; Purified genomic DNA from M.
              musculus C57BL/6J (male) was obtained from the Jackson
              Laboratory Mouse DNA Resource
              (http://www.jax.org/resources/documents/dnares/). The DNA
              was hydrodynamically sheared by repeated passage through a
              0.005 inch orifice at constant velocity. The sheared DNA
              was blunt end-repaired with T4 DNA polymerase and T4
              polynucleotide kinase. Adaptor oligonucleotides were
              ligated to the blunt ends in high molar excess. The
              adaptor DNA was purified and size-selected for a 9.5 to
              10.5 kb range using preparative agarose gel
              electrophoresis. Vector DNA was prepared from a derivative
              of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
              inducible derivative of plasmid R1. The vector was ligated
              with adaptors complementary to the insert adaptors and
              purified. The sheared, adaptor mouse DNA was annealed to
              adaptor vector DNA, and transformed into
              chemically-competent E. coli XL10-Gold (Stratagene) cells
              and selected for ampicillin resistance."
              Query Match      0.3%; Score 20.4; DB 1; Length 22;
              Best Local Similarity 95.5%; Pred. No. 1.9e+02;
              Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy  4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
          |||||
Db    1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 345
LOCUS    AZ463503
DEFINITION AZ463503 22 bp DNA linear GSS 04-OCT-2000
clone UUGC1M0272E24 F, genomic survey sequence.
ACCESSION AZ463503
VERSION    AZ463503.1 GI:10621628
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0142 row: 1 column: 24  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 22.

## FEATURES

Source

## source

source

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Class: plasmids
High quality sequence stop: 22.
Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0207D13"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

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Query Match          0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 1.9e+02;
Matches 21: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
and selected for ampicillin resistance.

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Qy 4464 TTTTTTTTTTTTTTTTTTTTGT 4485  
pb 1 TTTTTTTTTTTTTTTTTTTTTT 22

RESULT	360
AZ946102/c	
LOCUS	
DEFINITION	AZ946102 22 bp DNA linear GSS 27-APR-2001 M0207D13R Mouse 10kb plasmid UGUC2M library Mus musculus genomic clone UGUC2M0207D13 R, genomic survey sequence.
ACCESSION	AZ946102
VERSION	AZ946102.1 GI:13812911
KEYWORDS	GSS.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE  
AUTHORS  
1 (bases 1 to 22)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

```

Query Match      0.3%; Score 20.4; DB 1; Length 22;
Best Local Similarity 95.3%; Pred. No. 1.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTTGT 4485
      |||||
Db 22 TTTTTTTTTTTTTTTTTTTTTT 1
      |||||

```

RESULT 361	TA131B09P	22 bp	DNA	linear	GSS 13-DEC-2000
LOCUS	TA131B09P/c				
DEFINITION	T. brucei sheared genomic DNA clone 131b09, forward sequence, genomic survey sequence.				
ACCESSION	AL464164				
VERSION	AL464164.1	GI:11834427			
KEYWORDS	GSS.				
SOURCE	Trypanosoma brucei				
ORGANISM	Trypanosoma brucei				
	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;				
REFERENCE	1 (bases 1 to 22)				
AUTHORS	Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk				
COMMENT	Constructed at the Institute for Genomic Research (TIGR),				

COMMENT

Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of *Trypanosoma brucei* (TREU27/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (  $\lambda$  phage size) and ligated into a  $\lambda$  phage vector to give a tight size distribution ( 4 kb). The  $\lambda$  phage was used for the library construction as described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.

RESULT 363  
TA35C120



<b>DEFINITION</b>					
HD--09-K06.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (H <sup>+</sup> ) Oryza sativa cDNA clone HD--09-K06, mRNA sequence.					
<b>ACCESSION</b>					
CF319212.1 GI:33690973					
<b>VERSION</b>					
CF319212.1					
<b>KEYWORDS</b>					
EST.					
<b>SOURCE</b>					
<b>ORGANISM</b>					
Oryza sativa					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.					
<b>REFERENCE</b>					
<b>AUTHORS</b>					
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.					
<b>TITLE</b>					
Large-scale Sequencing Analysis of Rice ESTs					
<b>JOURNAL</b>					
Unpublished (2003)					
<b>COMMENT</b>					
Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myungji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.					
<b>FEATURES</b>					
<b>source</b>					
1..23					
Location/Qualifiers					
organism="Oryza sativa"					
mol_type="mRNA"					
cultivar="Nackdong"					
db_xref="taxon:4530"					
clones="HD-09-K06"					
tissue_type="callus"					
dev_stages="proliferated callus on 2N6 media for 2 weeks"					
lab_hosts="E.coli DH10B"					
clone_lib="OSHDAc1-overexpressing transgenic rice plasmid cDNA library (HD)"					
note="vector: pCR4-TOP0; Site 1: EcoRI; Callus was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."					
Query Match                 0.3%; Score 20.4; DB 1; Length 23;					
Best Local Similarity     95.5%; Pred.No. 2.e+02;					
Matches   21; Conservative   0; Mismatches   1; Indels   0; Gaps   0					
<b>QY</b> 4464 TTTTTCCTTTTTTTTTTTTTTTGT 4485					
<b>Db</b> 1 TTTTTCCTTTTTTTTTTTTTTTT 22					
<b>RESULT 370</b>					
CF322953/c					
<b>LOCUS</b>					
<b>DEFINITION</b>					
HDN--02-109.g1 OshDAC1-overexpressing transgenic rice lambda phage cDNA library II (HDN) Oryza sativa cDNA clone HDN--02-109, mRNA sequence.					
<b>ACCESSION</b>					
CF322953					
<b>VERSION</b>					
CF322953.1 GI:33794126					
<b>KEYWORDS</b>					
EST.					
<b>SOURCE</b>					
<b>ORGANISM</b>					
Oryza sativa					
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.					
<b>REFERENCE</b>					
<b>AUTHORS</b>					
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.					
<b>TITLE</b>					
Large-scale Sequencing Analysis of Rice ESTs					
<b>JOURNAL</b>					
Unpublished (2003)					
<b>COMMENT</b>					
Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myungji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193					

Fax: 82 31 321 6355  
Email: [bhnam@ggbio.com](mailto:bhnam@ggbio.com), [bhnam@bio.myongji.ac.kr](mailto:bhnam@bio.myongji.ac.kr).

**FEATURES**  
**source**

```

1. .23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/cisone="HDN-02-109"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.Coli SOLR"
/clone_lib="OSHACI-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5', end with EcoRI and 3', end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

```

```
Query Match          0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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[illegible]

RESULT 371	CF329042/c	CF329042	23 bp	mRNA	linear	EST 18-AUG-2003
LOCUS		NACL--04-D14.g1	Rice callus	plasmid	cDNA library	
DEFINITION		sativa cDNA	clone NACL--04-D14,		mRNA sequence.	
ACCESSION		CF329042				
VERSION		CF329042.1	GI:33806320			
KEYWORDS		EST.				

SOURCE	ORGANISM	PHYLOGENETIC ANALYSIS
Oryza sativa	Oryza sativa	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CONTACT: NAMM B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@qbio.com, bhnahm@bio.myonaj.ac.kr.

## FEATURES source

```

1. .23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clones="NACL--04-D14"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 30 days"
/lab_host="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/note="vector: PCR4-TOPO; Site_: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

```

```
Query Match          0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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**Qy**      4464 TTTT...TTTTTTGT 4485  
          |||||  
**Db**      23 TTTT...TTTTTTT 2

RESULT 372  
CF334657/C

LOCUS	CF334657	23 bp	mRNA	linear	EST 18-AUG-2003
DEFINITION	JMT-04-A14.g1 ATMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT-04-A14, mRNA sequence.				
ACCESSION	CF334657				
VERSION	CF334657.1	GI:33817648			
KEYWORDS	EST.				

SOURCE	ORGANISM
Oryza sativa	Oryza sativa
Oryza sativa	Oryza sativa

**REFERENCE** 1 (bases 1 to 23)

*Oryza sativa*  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CONTACT: NAMJUN B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.myongji.ac.kr.

## FEATURES

```
1. 23
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Naxdong"
/db_xref="taxon:4530"
/clone="JMT--04-A14"
/tissue_type="leaf"
/dev_stage="14 days after
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/dev, stages=14 days after germination".
/ab_host="E.coli DH10B"
/clone_lib="Atbmt-overexpressing transgenic rice plasmid
cDNA library (JMT)"
/note="Vector: pCRA-TOPO; Site 1: EcoRI; Oligo-capped mRNA
was reverse transcribed and then used for PCR. mRNA was
prepared from Arabidopsis Jaominate Carboxyl
methyltransferase overexpression line."

```

Query Match 0.3%; Score 20.4; DB 1; Length 23;  
Best Local Similarity 95.5%; Pred. No. 2.2e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0;  
Gaps 0;

**Qy**      4464 TTTTITTTTTTTTTTTTGT 4485  
          |  
**pB**      23 TTTTITTTTTTTTTTTTTT 2

RESULT 373  
AZ309219

LOCUS	AZ309219	23 bp	DNA	linear	GSS 29-SEP-2000
DEFINITION	IM0013G08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0013G08 F, genomic survey sequence.				

AZ309219  
 AZ309219.1  
 GI:10349986

VERSION 42303212.1 Q1:10549586  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus  
1 (bases 1 to 23)  
REFERENCE  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D., Weiss,R.  
1998







University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0089 row: D column: 19  
Seq primer: CTTGTAAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

**FEATURES**  
**source**

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1. 23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strains="C57BL/6J"
/db_xref="taxon:10090"
/clones="UUCG1M0089D19"
/sex="Male"
/lab_host="E. Coli strain"
/clone_libs="Mouse 10kb p"
/note="vector: PWD42nv;
musculus C57BL/6J (male)
Laboratory Mouse DNA Res
```

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1473214|gB|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* X110-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels
```

Qy 4464 TTTTTTTTTTTTTTTTGT 4485  
Dp 23 TTTTTTTTTTTTTTTTTT 2

RESULT 378  
A2357645/C

LOCUS	Accession	Size	Library	Species	Accession
DEFINITION	AZ357645	23 bp	DNA	linear	GSS 02-OCT-2000
LOCUS	IM0099C23F	Mouse 10kb	plasmid	UUGC1M library	Mus musculus genomic
DEFINITION	clone UUGC1M0099C23 F,				genomic survey sequence.

ACCESSION  
AZ357645

VERSION  
AZ357645.1 GI:10471345

KEYWORDS  
SOURCE  
Mus musculus (house mouse)  
GSS.

ORGANISM	Mus musculus
Source	Male maculae

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 21)

REFERENCE  
AUTHORS

1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 1000 Std Error: 0.00  
Plate: 0099 row: C column: 23  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

## FEATURES

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0099C23"
/sex="Male"
/lab_host="E. Coli strain"
/clone_lib="Mouse 10kb phage"
/note="Vector: PWD42nv;
musculus C57BL/6J (male)
Laboratory Mouse DNA res"

```

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [Gi/4732114 [9b]AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XU10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 23;  
Best Local Similarity 95.5%; Pred. No. 2.2e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels

Qy 4464 TTTTTTTTTTTTTTTTGT 4485  
 |||||  
 pb 23 TTTTTTTTTTTTTTTTTTTT 2

RESULT 379  
AZ419236

LOCUS	AZ419236	23 bp	DNA	linear	GSS 03-OCT-2000
DEFINITION	lmo195H07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0195H07 R, genomic survey sequence.				

ACCESSION AZ419236  
VERSION AZ419236.1 GI:10543249

KEYWORDS  
SOURCE  
GSS.  
Mus musculus (house mouse)

SOURCE	Mus musculus
ORGANISM	Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
1 (bases 1 to 23)

REFERENCE  
AUTHORS  
1 (bases 1 to 23)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Neiderhausen, A. and Wright, D., Weiss, R.

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

**JOURNAL**  
**Unpublished (20**  
**Praxis Index**

**COMMENT**  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah



FEATURES	FEATURES	source
High quality sequence stop: 23.	Location/Qualifiers	
High quality sequence stop: 23.	1	1
High quality sequence stop: 23.	23	23

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF139072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor-mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* X10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 23;  
Best Local Similarity 95.5%; Pred. No. 2.2e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy**      4464 TTTT TTTTTTTTTTTTTTTGT 4485  
          | | | | | | | | | | | | | |  
**pB**      1 TTTT TTTTTTTTTTTTTTTTTTT 22

RESULT 383	AZ588254	23 bp	DNA	linear	GSS 13-DEC-2000
LOCUS	AZ588254				
DEFINITION	1M0396024F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0396024 F, genomic survey sequence.				
ACCESSION	AZ588254				
VERSION	AZ588254.1	GI:11710444			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				

REFERENCE	1 (bases 1 to 23)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)

Niedenausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 1000 Std Error: 0.00  
Plate: 0396 row: 0 column: 24  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

## FEATURES

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1. 23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/_clone="UUGC1M0396O24"
sex="Male"
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ack-hosts="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/lab\_hosts="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGClon library"  
/notes="Vector: PWD42n; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gil4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 23;  
Best Local Similarity 95.5%; Pred. No. 2.2e+02;  
Matches 21: Conservative 0; Mismatches 1; Indels

QY 4464 TTTTTTTTTTTTTTTTTTGT 4485  
|||  
Db 1 TTTTTTTTTTTTTTTTTTTTTT 22

RESULT 384

AZ593540	23 bp DNA linear	GSS 13-DEC-2000
AZ593540	1M0495C07F Mouse 10kb plasmid UGCGIM library	Mus musculus genomic
DEFINITION	clone UGCGIM0495C07 F, genomic survey sequence.	
ACCESSION	AZ593540	
VERSION	AZ593540.1	GI:11715730
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	

ORGANISM Males and females

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus  
 1 (bases 1 to 23)  
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE	JOURNAL
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Unpublished (2000)

COMMENT  
Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu

Insert Length: 1000    Std Error: 0.00  
Plate: 0405 row: C column: 07  
Seq primer: CGTTGTAACACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 23.

## FEATURES

## source

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0405C07"
/sex="Male"
/lab_host="E. Coli strain Xl10-Gold, T1-resistant, P-"
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/clone lib="Mouse 10kb plasmid UUG1M library"

/note="Vector: PWD42 (male); Purified genomic DNA from M. musculus C57BL/6J was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli Xl10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 23;  
Best Local Similarity 95.5%; Pred. No. 2.2e+02;  
Matches 21: Conservative 0; Mismatches 1; Indels

**QY.**            4464 TTTTITTTTTTTTTTTTTGT 4485  
                |  
**pB**             1 TTTTITTTTTTTTTTTTTTTT 22

DEC 11 1955

LOCUS	AZ610785	23 bp	DNA	linear	GSS 13-DEC-2000
DEFINITION	IM0436N07F Mouse 10kb plasmid UGCGIM library Mus musculus genomic clone UUGCGIM0436N07 F. genomic survey sequence.				

ACCESSION  
AZ610785

RECESSION  
VERSION  
AZ610785.1  
GI:11732975

## KEYWORDS

Source: *Mus musculus* (house mouse)

SOURCE  
ORGANISM  
Muss musculus  
Muss musculus

ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
REFERENCE	1 (bases 1 to 23)

REFERENCE  
I (pages 1 to 23)  
AUTHORS  
Dunn D. Alvagi A. Barber

ADAMS, D., ROYAL, A., BARBER, M., BEACON, R., DAVIS, B., HAMILL, C., ISLAM, H., LONGACRE, S., MAHMOUD, M., MEENEN, E., PEDERSEN, T., REILLY, M., ROSE, M., ROSE, R., STOKES, R., TINGEY, A., von NIEDERTHAUSERN, A., and WRIGHT, D. WEISS, R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kbp  
paired reads and reads from 10kbp  
plasmid inserts

## JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss

## University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84142, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0514    row: E    column: 09  
Seq primer: CGTTGTAAACGACGCCAGT



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/mol_type="genomic DNA"
/~
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0033C07"
sex="male"
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/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UGIC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57Bl/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource"

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 23;  
Best Local Similarity 95.5%; Pred. No. 2.2e+02;

**Qy**      4464 TTTT TTTTTTTTTTTTTTTTGT 4485  
          ||| ||||||| | | | | |  
**pB**      23 TTTT TTTTTTTTTTTTTTTT 2

RESULT	391
AZ792751	
LOCUS	AZ792751 23 bp DNA linear GSS 16-FEB-2001
DEFINITION	2M0045K24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0045K24 F. genomic survey sequence.

VERSION AZ792751.1 GI:12937005  
KEYWORDS GSS.

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE  
AUTHORS  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
TITLE

**JOURNAL**  
Unpublished (2000)  
plasmid inserts

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606

Fax: 801 585 7177  
 Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0045 row: K column: 24  
 Seq primer: CGTGTAAACGACGGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 23.  
 Location/Qualifiers  
     1..23  
 FEATURES  
     source

**FEATURES**  
**SOURCE**

/organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC2M0045K24"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCIM library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G1|4732114|gb|Arl29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.3%	Score 20.4; DB 1; Length 23;
Best Local Similarity	95.5%	Pred. No. 2.2e+02;

Matches	21;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0
QY	4464	TTTTTTTTTTTTTTTTTTTT	TGT	4485					

RESULT 392  
AZ801003/c  
LOCUS  
AZ801003 23 bp DNA linear GSS 16-FEB-2001  
3M00591123 Mouse 10th plasmid library Mus musculus genomic  
DESCRIPTOR

DEFINITION  
clone UGC2.M0059J16 F, genomic survey sequence.  
ACCESSION  
AZ801003  
VERSION  
AZ801003.1 GI:12953326  
KEYWORDS  
genome

**KEYWORDS**  
GSS.  
Mus. muscululus (house mouse)  
SOURCE

SOURCE: Mus musculus (mouse)  
Mus musculus (mouse)  
Mus musculus (mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Island, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, P., Stokes, P., Tingey, A., von

Kelly, M., Rose, M., Rose, R., Stokes, R.,  
 Niederhausen, A. and Wright, D., Weiss, R.  
 Mammalian embryo development with and  
 without maternal effects. *Journal of*

# TITLE

## Mouse whole genome scaffolding with paired end reads from RAD

### plasmid inserts

**JOURNAL:** Unpublished (2000)  
**COMMENT:** Contact: Robert B. Weiss

University of Utah Genome Center  
University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
Tel: 801 585 5606

Fax: 801 585 7177  
Email: [cdunn@genetics.utah.edu](mailto:cdunn@genetics.utah.edu)

Insert Length: 10000    Std Error: 0.00  
Plate: 0059    row: J    column: 16

Lane: 0003  
 Row: 0  
 Column: 10  
 Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends  
High quality sequence stop: 23.

FEATURES	Location/Qualifiers
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/organism="Mus musculus"
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/clone="UUGC2M0165B14"
/sex="Male"
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/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4483
| | | | | | | | | | | | | | | | | | | | | |
Db 22 AATTTTTTTTTTTTTTTTTT 1

RESULT 394
AZ859570/c
LOCUS
DEFINITION
2M0165B14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0165B14 F, genomic survey sequence.
ACCESSION
AZ859570
VERSION
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: B column: 14
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/db_xref="taxon:10090"
/clone="UUGC2M0165B14"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4483
| | | | | | | | | | | | | | | | | | | | | |
Db 22 AATTTTTTTTTTTTTTTTTT 1

RESULT 394
AZ859570/c
LOCUS
DEFINITION
2M0165B14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0165B14 F, genomic survey sequence.
ACCESSION
AZ859570
VERSION
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0165 row: B column: 14
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
1..23
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

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/clone="UUGC2M0198107"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
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/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTTTGT 4485
      |||||||
Db 23 TTTTTTTTTTTTTTTTTTTT 2

RESULT 396
BH000534
LOCUS      23 bp DNA linear GSS 27-APR-2001
DEFINITION      2M0288B03R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0288B03 R, genomic survey sequence.
ACCESSION      BH000534
VERSION        BH000534.1 GI:13871760
KEYWORDS       GSS.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23)
Islam,D., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0288 row: B column: 03
Seq primer: CACACGAGAAACACTATGACC
Class: plasmid ends
High quality sequence stop: 23.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0288B03"

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/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTTTTTTTTTTTTTTTTTGT 4485
      |||||||
Db 1 TTTTTTTTTTTTTTTTTTTT 22

RESULT 397
TA151C02Q/c
LOCUS      23 bp DNA linear GSS 13-DEC-2000
DEFINITION      T. brucei sheared genomic DNA clone 151c02, reverse sequence,
genomic survey sequence.
ACCESSION      AL473028
VERSION        AL473028.1 GI:11838301
KEYWORDS       GSS.
SOURCE         Trypanosoma brucei
ORGANISM       Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 23)
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Ackin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
rhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: rnelayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1..23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="151c02"

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FEATURES  
source

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Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTTTTGT 4485
DB 23 TTTT...TTTTTTT 2

RESULT 398
TA274B03P
LOCUS TA274B03P
DEFINITION T. brucei sheared genomic DNA clone 274B03, forward sequence,
genomic survey sequence.
ACCESSION AL494584
VERSION AL494584.1 GI:11851281
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosomatidae; Kinetoplastida; Trypanosomatidae;
Eukaryota; Euglenozoa;
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
DIRECT SUBMISSION
TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
source
1. .23
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/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="353a10"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTTTTGT 4485
DB 23 TTTT...TTTTTTT 2

RESULT 400
AZ438069/c
LOCUS AZ438069
DEFINITION 1M0228A10F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0228A10 F, genomic survey sequence.
ACCESSION AZ438069
VERSION AZ438069.1 GI:10562178
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0228 row: A column: 10
Seq primer: CGTTGTAAACAGCCGCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
source
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTTTTGT 4485
DB 1 TTTT...TTTTTTT 22

RESULT 399
TA353A10P/c
LOCUS TA353A10P
DEFINITION T. brucei sheared genomic DNA clone 353a10, forward sequence,
genomic survey sequence.
ACCESSION AL494456
VERSION AL494456.1 GI:11870913
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosomatidae; Kinetoplastida; Trypanosomatidae;
Eukaryota; Euglenozoa;
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
DIRECT SUBMISSION
TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
source
1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274b03"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTTTTGT 4485
DB 1 TTTT...TTTTTTT 22

RESULT 399
TA353A10P/c
LOCUS TA353A10P
DEFINITION T. brucei sheared genomic DNA clone 353a10, forward sequence,
genomic survey sequence.
ACCESSION AL494456
VERSION AL494456.1 GI:11870913
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosomatidae; Kinetoplastida; Trypanosomatidae;
Eukaryota; Euglenozoa;
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
DIRECT SUBMISSION
TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
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Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
source
1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274b03"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTTTTGT 4485
DB 1 TTTT...TTTTTTT 22

RESULT 399
TA353A10P/c
LOCUS TA353A10P
DEFINITION T. brucei sheared genomic DNA clone 353a10, forward sequence,
genomic survey sequence.
ACCESSION AL494456
VERSION AL494456.1 GI:11870913
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosomatidae; Kinetoplastida; Trypanosomatidae;
Eukaryota; Euglenozoa;
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
DIRECT SUBMISSION
TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
source
1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274b03"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTTTTGT 4485
DB 1 TTTT...TTTTTTT 22

RESULT 399
TA353A10P/c
LOCUS TA353A10P
DEFINITION T. brucei sheared genomic DNA clone 353a10, forward sequence,
genomic survey sequence.
ACCESSION AL494456
VERSION AL494456.1 GI:11870913
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosomatidae; Kinetoplastida; Trypanosomatidae;
Eukaryota; Euglenozoa;
REFERENCE 1 (bases 1 to 23)
AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
DIRECT SUBMISSION
TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
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to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
Location/Qualifiers
source
1. .23
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="274b03"

Query Match      0.3%; Score 20.4; DB 1; Length 23;
Best Local Similarity 95.5%; Pred. No. 2.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTT...TTTTTTTGT 4485
DB 1 TTTT...TTTTTTT 
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0228A10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (G1|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 24;
Best Local Similarity 95.5%; Pred. No. 2.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACATTTTATTTTATTTTATTTT 4483
Db 23 ATTTTATTTTATTTTATTTT 2

RESULT 401
CF317007
LOCUS
DEFINITION
HD--06-114.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--06-114, mRNA sequence.
CF317007
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..25
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--06-114"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.Coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was

CF317007
25 bp mRNA linear EST 15-AUG-2003
HD--06-114.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--06-114, mRNA sequence.
CF317007
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..25
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--06-114"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.Coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"
/note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was

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treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was derived from rice Histone Deacetylase overexpression line."

Query Match      0.3%; Score 20.4; DB 1; Length 25;
Best Local Similarity 95.5%; Pred. No. 2.6e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTATTTTATTTTATTTTATTTTGT 4485
Db 1 TTTTATTTTATTTTATTTTATTTT 22

RESULT 402
CF299646
LOCUS
DEFINITION
7LEAF--03-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-L24, mRNA sequence.
CF299646
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match      0.3%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 2.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTATTTTATTTTATTTTATTTTGT 4485
Db 1 TTTTATTTTATTTTATTTTATTTT 22

RESULT 403
R26779
LOCUS
DEFINITION
Yh44f06.s1 Soares placenta Nb2Hp Homo sapiens cDNA clone IMAGE:132611.3; similar to gb:M85164 SERUM RESPONSE FACTOR ACCESSORY PROTEIN 1A (HUMAN); mRNA sequence.
R26779
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)

```

**ORGANISM**  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 26)

**REFERENCE**  
**AUTHORS**  
Hillier, L., Clark, N., Dubucque, T., Elliston, K., Hawkins, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lemon, G., Marra, M.,  
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
Insert Size: 1384  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LNL  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality  
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Seq primer: Promega -21ml3  
High quality sequence stop: 1.

**FEATURES**  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/sex="Female"  
/dev\_stage="placenta obtained at birth (full term)"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares placenta NB2HP"  
/note="Organ: placenta; Vector: pT7T3D (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; let  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
AAGTGAAGATTCGCGCCGAGAAATTTTTTTTTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified pT7T3 vector. Library  
went through one round of normalization. Library  
constructed by Bento Soares and M. Fatima Bonaldo."

Query Match 0.3%; Score 20.4; DB 1; Length 26;  
Best Local Similarity 95.5%; Pred. No. 2.9e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 4464 TTTTCTTTTCTTTTCTTTTCT 4485  
1 TTTTCTTTTCTTTTCTTTTCT 22

**Db**

**RESULT 404**  
**CNS00BGV**  
**LOCUS** 26 bp DNA linear GSS 04-JUN-1999  
**DEFINITION** Drosophila melanogaster genome survey sequence TET3 end of BAC #  
BACR23F05 of RP11-98 library from Drosophila melanogaster (fruit  
fly), genomic survey sequence.  
**ACCESSION** AL057060  
**VERSION** AL057060.1 GI:4937627  
**KEYWORDS** GSS.  
**SOURCE** Drosophila melanogaster (fruit fly)  
**ORGANISM** Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
1 (bases 1 to 26)  
/organism="Drosophila melanogaster"  
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/db\_xref="taxon:7227"  
/clone="BACR23F05"  
/clone\_lib="RP11-98"  
/note="end: TET3"

**Query Match** 0.3%; Score 20.4; DB 1; Length 26;  
**Best Local Similarity** 95.5%; Pred. No. 2.9e+02;  
**Matches** 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 4464 TTTTCTTTTCTTTTCTTTTCT 4485  
1 TTTTCTTTTCTTTTCTTTTCT 22

**Db**

**RESULT 404**  
**CNS00BGV**  
**LOCUS** 26 bp DNA linear GSS 13-DEC-2000  
**DEFINITION** T. brucei sheared genomic DNA clone 32lg11, forward sequence,  
Genomic survey sequence.  
**ACCESSION** AL492371  
**VERSION** AL492371.1 GI:11867375  
**KEYWORDS** GSS.  
**SOURCE** Trypanosoma brucei  
Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.  
1 (bases 1 to 26)  
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU97/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).  
Location/Qualifiers  
1..26  
/organism="Trypanosoma brucei"

**QY** 4463 CTTTCTTTTCTTTTCTTTTCT 4486  
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**Db**

**FEATURES**  
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/clone="BACR23F05"  
/clone\_lib="RP11-98"  
/note="end: TET3"

**Query Match** 0.3%; Score 20.4; DB 1; Length 26;  
**Best Local Similarity** 87.5%; Pred. No. 2.9e+02;  
**Matches** 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

**QY** 4463 CTTTCTTTTCTTTTCTTTTCT 4486  
1 CTTTCTTTTCTTTTCTTTTCT 24

**Db**

**FEATURES**  
Location/Qualifiers  
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/clone="BACR23F05"  
/clone\_lib="RP11-98"  
/note="end: TET3"

**Query Match** 0.3%; Score 20.4; DB 1; Length 26;  
**Best Local Similarity** 87.5%; Pred. No. 2.9e+02;  
**Matches** 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

**QY** 4463 CTTTCTTTTCTTTTCTTTTCT 4486  
1 CTTTCTTTTCTTTTCTTTTCT 24

**Db**

**FEATURES**  
Location/Qualifiers  
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/db\_xref="taxon:7227"  
/clone="BACR23F05"  
/clone\_lib="RP11-98"  
/note="end: TET3"

**Query Match** 0.3%; Score 20.4; DB 1; Length 26;  
**Best Local Similarity** 87.5%; Pred. No. 2.9e+02;  
**Matches** 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

**QY** 4463 CTTTCTTTTCTTTTCTTTTCT 4486  
1 CTTTCTTTTCTTTTCTTTTCT 24

**Db**

**FEATURES**  
Location/Qualifiers  
1..26  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR23F05"  
/clone\_lib="RP11-98"  
/note="end: TET3"

**Query Match** 0.3%; Score 20.4; DB 1; Length 26;  
**Best Local Similarity** 87.5%; Pred. No. 2.9e+02;  
**Matches** 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

**QY** 4463 CTTTCTTTTCTTTTCTTTTCT 4486  
1 CTTTCTTTTCTTTTCTTTTCT 24

**Db**

**FEATURES**  
Location/Qualifiers  
1..26  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR23F05"  
/clone\_lib="RP11-98"  
/note="end: TET3"

**Query Match** 0.3%; Score 20.4; DB 1; Length 26;  
**Best Local Similarity** 87.5%; Pred. No. 2.9e+02;  
**Matches** 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

**QY** 4463 CTTTCTTTTCTTTTCTTTTCT 4486  
1 CTTTCTTTTCTTTTCTTTTCT 24

**Db**

**FEATURES**  
Location/Qualifiers  
1..26  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR23F05"  
/clone\_lib="RP11-98"  
/note="end: TET3"

**Query Match** 0.3%; Score 20.4; DB 1; Length 26;  
**Best Local Similarity** 87.5%; Pred. No. 2.9e+02;  
**Matches** 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

**QY** 4463 CTTTCTTTTCTTTTCTTTTCT 4486  
1 CTTTCTTTTCTTTTCTTTTCT 24

**Db**

**FEATURES**  
Location/Qualifiers  
1..26  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR23F05"  
/clone\_lib="RP11-98"  
/note="end: TET3"

**Query Match** 0.3%; Score 20.4; DB 1; Length 26;  
**Best Local Similarity** 87.5%; Pred. No. 2.9e+02;  
**Matches** 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

**QY** 4463 CTTTCTTTTCTTTTCTTTTCT 4486  
1 CTTTCTTTTCTTTTCTTTTCT 24

**Db**

**FEATURES**  
Location/Qualifiers  
1..26  
/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:7227"  
/clone="BACR23F05"  
/clone\_lib="RP11-98"  
/note="end: TET3"

**Query Match** 0.3%; Score 20.4; DB 1; Length 26;  
**Best Local Similarity** 87.5%; Pred. No. 2.9e+02;  
**Matches** 2

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/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="321911"

Query Match      0.3%; Score 20.4; DB 1; Length 26;
Best Local Similarity 95.5%; Pred. No. 2.9e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTGTGTGTGTGTGTGTGTGTGT 4483
Db 23 AATTTTGTGTGTGTGTGTGTGTGTGT 2

RESULT 406
N34459
LOCUS      27 bp      mRNA      linear      EST 16-JAN-1996
DEFINITION Y13C06.s1 Soares melanocyte 2NDHM Homo sapiens cDNA clone
IMAGE:271114 3' similar to gb:D00174 ALPHA-2-ANTIPLASMIN PRECURSOR
(HUMAN);, mRNA sequence.
ACCESSION  N34459
VERSION     N34459.1 GI:1155601
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 27)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevisakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
TITLE        The WashU-Merck EST Project
JOURNAL      Unpublished (1995)
COMMENT      Contact: Willson RK
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              High quality sequence stops: 16
              Source: IMAGE Consortium, LNL
              This clone is available royalty-free through LNL; contact the
              IMAGE Consortium (info@image.llnl.gov) for further information.
              Seq primer: ml3 -40 forward
              High quality sequence stop: 16.
FEATURES
  source
    1..27
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="GDB:3880756"
    /db_xref="taxon:9606"
    /clone="IMAGE:271114"
    /sex="Male"
    /tissue_type="melanocyte"
    /lab_host="DH10B (ampicillin resistant)"
    /clone_lib="Soares melanocyte 2NDHM"
    /note="Vector: p77T3D (Pharmacia) with a modified
    polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
    was primed with a Not I - oligo(dT) primer [5',
    TGTTACCACTGAGTGGAGCGCGCGAGTTTGTGTGTGTGTGT 3'],
    double-stranded cDNA was size selected, ligated to Eco RI
    adapters (Pharmacia), digested with Not I and cloned into
    the Not I and Eco RI sites of a modified p77T3 vector
    (Pharmacia). Library constructed by Bento Soares and
    M. Fatima Bonaldo. RNA from normal foreskin melanocytes
    (FS374) was kindly provided by Dr. Anthony P. Albino."

Query Match      0.3%; Score 20.4; DB 1; Length 27;
Best Local Similarity 95.5%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 4464 TTTTGTGTGTGTGTGTGTGTGTGTGT 4485
Db 1 TTTTGTGTGTGTGTGTGTGTGTGTGT 22

RESULT 407
T52979
LOCUS      27 bp      mRNA      linear      EST 06-FEB-1995
DEFINITION Y82e08.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone
IMAGE:68198 3' similar to gb:D00174 ALPHA-2-ANTIPLASMIN
PRECURSOR (HUMAN), mRNA sequence.
ACCESSION  T52979
VERSION     T52979.1 GI:654839
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 27)
AUTHORS     Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chisoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J.,
Trevisakis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
and Marra,M.
TITLE        Generation and analysis of 280,000 human expressed sequence tags
JOURNAL      Genome Res. 6 (9), 807-828 (1996)
MEDLINE     97044478
PUBMED      8889549
COMMENT      Other ESTs: Y82e08.t1
              Contact: Willson RK
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@watson.wustl.edu
              Insert Size: 577
              High quality sequence starts: 1 High quality sequence stops: 1
              Source: IMAGE Consortium, LNL This clone is available royalty-free
              through LNL; contact the IMAGE Consortium (info@image.llnl.gov)
              for further information. Trace considered overall poor quality
              Insert Length: 577 Std Error: 0.00
              Seq primer: -21ml3
              High quality sequence stop: 1.
FEATURES
  source
    1..27
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="GDB:504455"
    /db_xref="taxon:9606"
    /clone="IMAGE:68198"
    /sex="female"
    /dev_stage="49 year old"
    /lab_host="SOLR cells (kanamycin resistant)"
    /clone_lib="Stratagene ovary (#937217)"
    /note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;
    Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
    Total ovary tissue, normal, caucasian. Average insert
    size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
    GAATTCGGCAGCAG 3' -3' adaptor sequence: 5'
    CTCGAGTTTGTGTGTGTGTGTGTGTGT 3'"

Query Match      0.3%; Score 20.4; DB 1; Length 27;
Best Local Similarity 91.3%; Pred. No. 3.2e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTGTGTGTGTGTGTGTGTGTGTGT 4486
Db 3 TTTTGTGTGTGTGTGTGTGTGTGTGT 25

RESULT 408

```

LOCUS	AZ357605	28 bp	DNA	linear	GSS 02-OCT-2000
DEFINITION	1M0099115F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0099115 F, genomic survey sequence.				
ACCESSION	AZ357605				
VERSION	AZ357605.1	GI:10471305			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 28)				
	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D. Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Robert B. Weiss				
	University of Utah				
	University of Utah				
	Rm. 308 Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT				
	84112, USA				
	Tel: 801 585 5606				
	Fax: 801 585 7177				
	Email: ddunn@genetics.utah.edu				
	Insert Length: 10000	Std Error: 0.00			
	Plate: 0099	row: 1	column: 15		
	Seq primer: CGTTGTAAACGACGCCAGT				
	Class: plasmid ends				
	High quality sequence stop: 28.				
FEATURES	Location/Qualifiers				

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FEATURES             source
1. .28
/location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGClM0099I15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGClM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|732114|gb|AF129072.1), a copy-number was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match          0.3%; Score 20.4; DB 1; Length 28;
Best Local Similarity 95.5%; Pred. No. 3.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4462 ACTTTTTCCTTTTTTTTTTTTTTTT 4483
        | |||||
DB       22 AATTTTTCCTTTTTTTTTTTTTTTT 1

```

RESULTS	29 bp	mpNA	linear	EST 04-SRP-2003
AL048747/c				
AL048747				
LOCIS				

```

DEFINITION DKFZp566K043.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone
ACCESSION DKFZp566K043 mRNA sequence.
VERSION AL048747 GI:4727818
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 29)
AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.
FEATURES
    source
        1..29
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="DKFZp566K043"
            /tissue_type="kidney"
            /dev_stage="fetal"
            /lab_host="X1-2blue"
            /clone_lib="566 (synonym: hfkd2)"
            /note="vector: pAMPl; Site_1: NotI; Site_2: SalI"
Query Match 0.3%; Score 20.4; DB 1; Length 29;
Best Local Similarity 95.5%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4465 TTTTTCCTTTTTCCTTTTTCCT 4486
Db 29 TTTTTCCTTTTTCCTTTTTCCT 8
RESULT 411
BQ586486/c
LOCUS
DEFINITION E012391-024-012-J22-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
ACCESSION BQ586486
VERSION BQ586486.1 GI:26116068
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 29)
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 12 row: J column: 22
Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES
    source
        1..29
            /organism="Beta vulgaris"
            /mol_type="mRNA"
            /cultivar="KWS2320 (double haploid, monogerm breeding

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line)"
/db_xref="GABI:186373"
/db_xref="taxon:161934"
/clone="024-012-J22"
/tissue_type="leaf"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-leaf"
/note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
b.schulze@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCGCG-SP6-prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
Query Match 0.3%; Score 20.4; DB 1; Length 29;
Best Local Similarity 95.5%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 4466 TTTTTCCTTTTTCCTTTTTCCT 4487
Db 29 TTTTTCCTTTTTCCTTTTTCCT 8
RESULT 412
BX567540
LOCUS
DEFINITION BX567540 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse88f02_plc, mRNA sequence.
ACCESSION BX567540
VERSION BX567540.1 GI:33434463
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 29)
AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix gic are reverse primer reads starting at 5',
end of the cDNA all plc reads are from
the 3' end.
FEATURES
    source
        1..29
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /sub_species="morsitans"
            /db_xref="taxon:37546"
            /clone="Tse88f02_plc"
            /tissue_type="adult infected gut"
            /clone_lib="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucei"

```



CONTACT: ROBERT B. WEISS  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 10000 Std Error: 0.00  
Plate: 0100 row: N column: 08  
Seq primer: CGTTGTAACACGCGCCAGT  
Class: plasmid ends

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FEATURES
source
  High quality sequence stop: 29.
  Location/Qualifiers
    1..29
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UTGCM0100N08"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UGCM library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20.4; DB 1; Length 29;
Best Local Similarity 95.5%; Pred. No. 3.7e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4483
DB 23 ATTTTTTTTTTTTTTTTTTT 2

RESULT 416
TA378G07P
LOCUS      29 bp      DNA      linear      GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 378g07, forward sequence, genomic survey sequence.
VERSION    AL497621.1 GI:11873343
KEYWORDS   GSS.
SOURCE     Trypanosoma brucei
ORGANISM   Trypanosoma brucei
            Eukaryota; Euzoenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1 (bases 1 to 29)
AUTHORS    Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B. El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE      Direct Submission
JOURNAL    Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
COMMENT    Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
  Query Match      0.3%; Score 20.4; DB 1; Length 29;
  Best Local Similarity 95.5%; Pred. No. 3.7e+02;
  Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 TTTTGTGTTTGTGTTTGTGTTTGT 4485
DB 1 TTTTGTGTTTGTGTTTGTGTTTGT 22

RESULT 417
BE539470
LOCUS      30 bp      mRNA      linear      EST 09-AUG-2000
DEFINITION 601060134F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3446720 5', mRNA sequence.
ACCESSION  BE539470
VERSION    BE539470.1 GI:9768115
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 30)
AUTHORS    NIH-MGC http://mgi.nci.nih.gov/
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Email: cgabs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Incyte Genomics, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Plate: LLAM8419 row: c column: 09
            High quality sequence stop: 30.
            Location/Qualifiers
              1..30
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:3446720"
                /cell_line="MGC36"
                /lab_host="DH10B"
                /clone_lib="NIH MGC 10"
                /note="Organ: cervix; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.5 kb. Library prepared by Life Technologies."

Query Match      0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 52 GCGCGCAACGAGCTGCGGGCGCGCGCGC 81
DB 1 GCGCAGTACGCGGGCGCGCGCGTGGCGC 30

RESULT 418
BM280395
LOCUS      30 bp      mRNA      linear      EST 17-SEP-2002
DEFINITION 3'EST-NCD15-143 human CD15+ myeloid progenitor cells cDNA library
            Homo sapiens cDNA 3', mRNA sequence.
ACCESSION  BM280395

```

```

VERSION BM280395.1 GI:23025929
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Chen, J., Sun, M., Lee, S., Zhou, G., Rowley, J. D. and Wang, S. M.
TITLE Identifying novel transcripts and novel genes in the human genome
        by using novel SAGE tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (19), 12257-12262 (2002)
COMMENT Contact: Wang SM
        Hem/Onc
        University of Chicago Medical Center
        5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
        Tel: 773-702-6788
        Fax: 773-702-3002
        Email: swangl@midway.uchicago.edu
This EST fragment was amplified from human CD15+ myeloid progenitor
cells cDNA library with GLGI technique (Generation of Longer cDNA
fragments from SAGE tags for Gene Identification, Proc. Natl. Acad.
Sci. USA 97, 349, 2000). A high-throughput GLGI procedure for
converting a large number of SAGE tag sequences into 3' ESTs,
Genes, Chromosomes & Cancers, in press), which starts from the 3'
end till the last CARG site of the target cDNA sequence.
Seq primer: M13 Forward.
FEATURES
        source
            1..30
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /tissue_type="bone marrow"
            /cell_type="CD15+ myeloid progenitor cells"
            /clone_lib="human CD15+ myeloid progenitor cells cDNA
            Library"

Query Match 0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4467 TTTTCTTTTCTTTTCTTCTGACATG 4496
DB 1 TTTTCTTTTCTTTTCTTCTGACATG 30

RESULT 419
BX549675 30 bp mRNA linear EST 10-OCT-2003
LOCUS BX549675 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse109c08_pic, mRNA sequence.
ACCESSION BX549675
VERSION BX549675.1 GI:33368809
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 30)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
FEATURES
        source
            1..30
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /sub_species="morsitans"
            /db_xref="taxon:37546"
            /clone="Tse109c08_pic"
            /tissue_type="adult infected gut"
            /clone_lib="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucei"

School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
FEATURES
        source
            1..30
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /sub_species="morsitans"
            /db_xref="taxon:37546"
            /clone="Tse109c08_pic"
            /tissue_type="adult infected gut"
            /clone_lib="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucei"

Query Match 0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 95.5%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4483
DB 9 AGTTTCTTTTCTTTTCTTTTCTTTTCTTTT 30

RESULT 420
BX551003 30 bp mRNA linear EST 10-OCT-2003
LOCUS BX551003 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse116a06_pic, mRNA sequence.
ACCESSION BX551003
VERSION BX551003.1 GI:33374807
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 30)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
FEATURES
        source
            1..30
            /organism="Glossina morsitans morsitans"
            /mol_type="mRNA"
            /sub_species="morsitans"
            /db_xref="taxon:37546"
            /clone="Tse116a06_pic"
            /tissue_type="adult infected gut"
            /clone_lib="Glossina morsitans morsitans adult infected
            gut"
            /note="country: Zimbabwe; EST from adult gut infected with
            T.brucei"

```

```

T.brucei"

Query Match      0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 95.5%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTT...TTTTTTT 4483
Db 9 AGTTTT...TTTTTTT 30

RESULT 421
BX554779
LOCUS      BX554779      30 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION morsitans morsitans morbitans adult infected gut Glossina
VERSION    BX554779
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Hippoboscidae; Glossinidae; Glossina.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
           Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE      Adult midgut expressed sequence tags from the tsetse fly Glossina
           morsitans morsitans and expression analysis of putative immune
           response genes
JOURNAL    Genome Biol. 4 (10), R63 (2003)
MEDLINE    22881942
PUBMED     14519198
COMMENT    Contact: Hall N
           The Sanger Institute The Wellcome Trust Genome Campus
           Hinxton, Cambridge, CB10 1SA, UK
           Request for clones, please contact: Mike Lehane
           Prof. M.J.Lehane
           School of Biological Sciences,
           University of Wales,
           Bangor LL57 2UW
           All clones with suffix q1c are reverse primer reads starting at 5'
           end of the cDNA all pic reads are from
           the 3' end.

FEATURES             source
     source           1..30
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse22d06_pic"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /note="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

Query Match      0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 95.5%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTT...TTTTTTT 4483
Db 9 AGTTTT...TTTTTTT 30

RESULT 423
BX559425
LOCUS      BX559425      30 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION morsitans morsitans morbitans adult infected gut Glossina
VERSION    BX559425
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Hippoboscidae; Glossinidae; Glossina.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
           Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE      Adult midgut expressed sequence tags from the tsetse fly Glossina
           morsitans morsitans and expression analysis of putative immune
           response genes
JOURNAL    Genome Biol. 4 (10), R63 (2003)
MEDLINE    22881942
PUBMED     14519198
COMMENT    Contact: Hall N

T.brucei"

Query Match      0.3%; Score 20.4; DB 1; Length 30;
Best Local Similarity 95.5%; Pred. No. 4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTT...TTTTTTT 4483
Db 8 AGTTTT...TTTTTTT 29

RESULT 422
BX555710
LOCUS      BX555710      30 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION morsitans morsitans morbitans adult infected gut Glossina
VERSION    BX555710
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
           Hippoboscidae; Glossinidae; Glossina.
REFERENCE  1 (bases 1 to 30)
AUTHORS    Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
           Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE      Adult midgut expressed sequence tags from the tsetse fly Glossina
           morsitans morsitans and expression analysis of putative immune
           response genes
JOURNAL    Genome Biol. 4 (10), R63 (2003)
MEDLINE    22881942
PUBMED     14519198
COMMENT    Contact: Hall N

```

Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

## FEATURES

source  
1..30  
Location/Qualifiers

/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse43e07\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.3%; Score 20.4; DB 1; Length 30;  
Best Local Similarity 95.5%; Pred. No. 4e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4483

Db 9 AGTTTTTTTTTTTTTTTTT 30

## RESULT 424

BS563547  
LOCUS  
DEFINITION  
BX563547 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse67e03\_plc, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BS563547.1 GI:33430769  
EST.  
Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
1 (bases 1 to 30)

REFERENCE  
AUTHORS  
TITLE  
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL  
MEDLINE  
PUBMED

Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198

## COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

## FEATURES

source

1..30  
Location/Qualifiers

/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"

/clone="Tse67e03\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.3%; Score 20.4; DB 1; Length 30;  
Best Local Similarity 95.5%; Pred. No. 4e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4483

Db 9 AGTTTTTTTTTTTTTTTTT 30

## RESULT 425

BS565972  
LOCUS  
DEFINITION  
BX565972 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse7e12\_plc, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BS565972.1 GI:33433017  
EST.  
Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
1 (bases 1 to 30)

REFERENCE  
AUTHORS  
TITLE  
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL  
MEDLINE  
PUBMED

Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198

## COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

## FEATURES

source

1..30  
Location/Qualifiers

/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse7e12\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.3%; Score 20.4; DB 1; Length 30;  
Best Local Similarity 95.5%; Pred. No. 4e+02;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4483

Db 9 AGTTTTTTTTTTTTTTTTT 30

## RESULT 426

```

AW245279      AW245279      31 bp      mRNA      linear      EST 07-JAN-2000
LOCUS         2820044.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820044 3',
DEFINITION    mRNA sequence.
ACCESSION     AW245279
VERSION       AW245279.1  GI:6588272
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 31)
AUTHORS       NTH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Other ESTs: 2820044.5prime
               Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling
               Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
               Consortium (ILMI) DNA Sequencing by: Berkeley MGC sequencing
               project Clone distribution: MGC clone distribution information can
               be found through the I.M.A.G.E. Consortium/ILMI at:
               www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
               Scores: PHRED from University of Washington Genome Center. Vector
               Trimming: cross_match from University of Washington Genome Center
               PHRAP suite. Poly-T Identification: patmatch.pl from Berkeley
               Drosophila Genome Project. University of Washington Genome Center:
               http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
               PHRED high quality bases following vector sequence. Very Low
               Quality Sequence: Trace file contained 31 contiguous distinct peaks
               following vector sequence. Polyadenylation: Based upon the presence
               of a XhoI site followed by a run of 14 or more T residues at the
               beginning of the sequence, this cDNA insert was polyadenylated.
               Plate: LLCM3 row: C column: 21.
FEATURES             Location/Qualifiers
     source           1..31
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2820044"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_hosts="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5',
                     adaptor: GGCACGAG(G). Size-selected >500bp for average
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
```

```

Query Match      0.3%; Score 20.4; DB 1; Length 31;
Best Local Similarity 84.0%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4464 TTTT...TTT...TTT...TTT...TTT...TTT...TTT...TTT 4488
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      5 TTTT...TTT...TTT...TTT...TTT...TTT...TTT...TTT 29

Db

RESULT 427
BX554068
LOCUS         BX554068      31 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION    Glossina morsitans morsitans adult infected gut Glossina
               morsitans morsitans cDNA clone Tse13c01_plc, mRNA sequence.
ACCESSION     BX554068
VERSION       BX554068.1  GI:33378169
KEYWORDS      EST.
SOURCE        Glossina morsitans morsitans
               Glossina morsitans morsitans
```

```

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscidae; Glossinidae; Glossina.
REFERENCE     1 (bases 1 to 31)
AUTHORS       Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
               Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE         Adult midgut expressed sequence tags from the tsetse fly Glossina
               morsitans morsitans and expression analysis of putative immune
               response genes
JOURNAL       Genome Biol. 4 (10), R63 (2003)
MEDLINE       22881942
PUBMED        14519198
COMMENT       Contact: Hall N
               Pathogen Sequencing Unit
               The Sanger Institute The Wellcome Trust Genome Campus
               Hinxton, Cambridge, CB10 1SA, UK
               Request for clones, please contact: Mike Lehane
               Prof. M.J.Lehane
               School of Biological Sciences,
               University of Wales,
               Bangor LL57 2UW
               All clones with suffix q1c are reverse primer reads starting at 5'
               end of the cDNA all plc reads are from
               the 3' end.
FEATURES             Location/Qualifiers
     source           1..31
                     /organism="Glossina morsitans morsitans"
                     /mol_type="mRNA"
                     /sub_species="morsitans"
                     /db_xref="taxon:37546"
                     /clone="Tse13c01_plc"
                     /tissue_type="adult infected gut"
                     /clone_lib="Glossina morsitans morsitans adult infected
                     gut"
                     /notes="country: Zimbabwe; EST from adult gut infected with
                     T.brucei"

Query Match      0.3%; Score 20.4; DB 1; Length 31;
Best Local Similarity 95.5%; Pred. No. 4.3e+02;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTT...TTT...TTT...TTT...TTT...TTT...TTT...TTT 4483
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
      9 AGTTT...TTT...TTT...TTT...TTT...TTT...TTT...TTT 30

Db

RESULT 428
BX557470
LOCUS         BX557470      31 bp      mRNA      linear      EST 10-OCT-2003
DEFINITION    Glossina morsitans morsitans adult infected gut Glossina
               morsitans morsitans cDNA clone Tse32f01_plc, mRNA sequence.
ACCESSION     BX557470
VERSION       BX557470.1  GI:33428655
KEYWORDS      EST.
SOURCE        Glossina morsitans morsitans
               Glossina morsitans morsitans
ORGANISM      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
               Hippoboscidae; Glossinidae; Glossina.
REFERENCE     1 (bases 1 to 31)
AUTHORS       Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
               Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE         Adult midgut expressed sequence tags from the tsetse fly Glossina
               morsitans morsitans and expression analysis of putative immune
               response genes
JOURNAL       Genome Biol. 4 (10), R63 (2003)
MEDLINE       22881942
PUBMED        14519198
COMMENT       Contact: Hall N
               Pathogen Sequencing Unit
               The Sanger Institute The Wellcome Trust Genome Campus
               Hinxton, Cambridge, CB10 1SA, UK
               Request for clones, please contact: Mike Lehane
```

	/note="country: Zimbabwe; EST from adult gut infected with T.brucei"	
--	--	--

Query Match                  0.3%; Score 20.4; DB 1; Length 31;  
Best Local Similarity      95.5%; Pred. No. 4.3e+02;  
Matches    21; Conservative    0; Mismatches    1; Indels     0; Gaps       0;

  

OY      4462 ACTTTTTTTTTTTTTTTTTTTT 4483  
| | | | | | | | | | | | | |  
Db      9 AGTTTTTTTTTTTTTTTTTTTTT 30

  
  

RESULT 430  
BX559254 LOCUS  
DEFINITION Glossina morsitans morisitans cdna clone Tse42e03\_plc, mRNA sequence.  
ACCESSION BX559254  
VERSION BX559254.1 GI:33366505  
KEYWORDS EST.  
SOURCE Glossina morsitans morisitans  
ORGANISM Glossina morsitans morisitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.  
REFERENCE 1 (bases 1 to 31)  
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kethornou,A., Berriman,M., Hamilton,J., Soares,M.B., Ronaldo,M.F., Lehanne,S. and Hall,N.  
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morisitans and expression analysis of putative immune response genes  
JOURNAL Genome Biol. 4 (10), R63 (2003)  
MEDLINE 22881942  
PUBMED 14519198  
COMMENT Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinnton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
source location/Qualifiers  
1..31 /organism=Glossina morsitans morisitans"  
/mol\_type="mRNA"  
/sub\_species="morisitans"  
/db\_xref=taxon:37546"  
/clone=Tse42e03\_plc"  
/tissue type=adult infected gut"  
clone\_lib=Glossina morsitans morisitans adult infected gut"  
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

  

Query Match                  0.3%; Score 20.4; DB 1; Length 31;  
Best Local Similarity      95.5%; Pred. No. 4.3e+02;  
Matches    21; Conservative    0; Mismatches    1; Indels     0; Gaps       0;

  

OY      4462 ACTTTTTTTTTTTTTTTTTTTT 4483  
| | | | | | | | | | | | | |  
Db      9 AGTTTTTTTTTTTTTTTTTTTTT 30

  
  

RESULT 431  
CF296152 LOCUS  
DEFINITION CF296152 32 bp mRNA linear EST 14-AUG-2003  
sativa cDNA clone 30DGS--06-G09\_ b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--06-G09\_ mRNA sequence.











```

/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0220B08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.3%; Score 20.2; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 4464 TTTTTCCTTTTTCCTTTCCTT 4488
      ||||||| ||||||| |||
Db 27 TTTTTCCTTTTTCCTTTCCTT 3

```

```

RESULT 441
AZ458228/c
LOCUS
DEFINITION
  AZ458228 Mouse 10kb plasmid UUCG1M library Mus musculus genomic
  clone UUCG1M0262C12 F, genomic survey sequence.
ACCESSION
  AZ458228
VERSION
  AZ458228.1 GI:10616353
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 27)
REFERENCE
  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
  Irlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
  Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
  Niederhausen,A. and Wright,D.,Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0262 row: C column: 12
  Seq primer: CGTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 27.
  Location/Qualifiers
    1..27
      /organism="Mus musculus"

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0262C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, P-"
/clone_lib="Mouse 10kb plasmid UUCG1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.3%; Score 20.2; DB 1; Length 27;
Best Local Similarity 88.0%; Pred. No. 3.4e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 4464 TTTTTCCTTTTTCCTTTCCTT 4488
      ||||||| ||||||| |||
Db 27 TTTTTCCTTTTTCCTTTCCTT 3

```

```

RESULT 442
AL587605
LOCUS
DEFINITION
  AL587605 BP Chicken Brain Library Gallus gallus cdna clone
  ROS059F11, mRNA sequence.
ACCESSION
  AL587605
VERSION
  AL587605.1 GI:13192639
KEYWORDS
  EST.
SOURCE
  Gallus gallus (chicken)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
  Phasianinae; Gallus.
  1 (bases 1 to 28)
REFERENCE
  Murray,F.
  BP Chicken Brain Library
  Unpublished (2001)
  Contact: Frazer Murray
  Dept. Genomics and Bioinformatics
  Roslin Institute
  Roslin, Midlothian, EH25 9PS, UK
  Tel: +44 (0)131 527 4200
  Fax: +44 (0)131 440 0434
  Email: frazer.murray@bbsrc.ac.uk
  CGGCGCGCTTTTTCCTTTCCTT 3' Poly A RNA purchased from Clontech
  (*6854-
  Seq primer: M13F.
  Location/Qualifiers
    1..28
      /organism="Gallus gallus"
      /mol_type="mRNA"
      /db_xref="taxon:9031"
      /clone="ROS059F11"
      /tissue type="Brain"
      /dev stage="Unknown"
      /lab_host="DH10B"
      /clone_lib="BP Chicken Brain Library"

```

/note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACTCGAG 3'; 3' adaptor sequence: 5' GCGGCGCTTTTTTTTTTTT 3'. Poly A RNA purchased from Clontech (\*6854-1)"

Query Match 0.3%; Score 20.2; DB 1; Length 28;  
Best Local Similarity 81.5%; Pred. No. 3.7e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
QY 4466 TTTTNTTTTTTTTTTTTCTTTGAGA 4492  
Db 1 TTTTNTTTTTTTTTTTTCTTTGAGA 27

RESULT 443  
AW332443 28 bp mRNA linear EST 31-JAN-2000  
LOCUS S8E7 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.  
DEFINITION AW332443  
ACCESSION AW332443  
VERSION AW332443.1 GI:6828800  
KEYWORDS EST.  
SOURCE Pneumocystis carinii  
ORGANISM Pneumocystis carinii  
Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;  
Pneumocystidaceae; Pneumocystis.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Smulian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,  
Edman,J.C., Kovacs,J. and Cushion,M.  
TITLE Expressed sequence tags from Pneumocystis carinii  
JOURNAL Unpublished (2000)  
COMMENT Contact: Staben C  
School of Biological Sciences  
University of Kentucky  
101 Morgan Building, University of Kentucky, Lexington, KY  
40506-0225, USA  
Tel: 606 257 2161  
Fax: 606 257 1717  
Email: staben@pop.uky.edu.

FEATURES  
source  
1..28  
/organism="Pneumocystis carinii"  
/mol\_type="mRNA"  
/db\_xref="taxon:4754"  
/lab\_host="E. coli"  
/clone\_lib="AGS-1"  
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;  
P. carinii organisms (3x10e9) from a single rat (99-1-6,  
sacrificed on 3/17/99) at Cincinnati VA facilities.  
Trizol extracted RNA. Oligo dt priming, standard  
conditions described by vendor, Stratagene. Further  
details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.3%; Score 20.2; DB 1; Length 28;  
Best Local Similarity 88.0%; Pred. No. 3.7e+02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 4464 TTTTNTTTTTTTTTTTTCTTTGCTT 4488  
Db 1 TTTTNTTTTTTTTTTTTCTTTGCTT 25

RESULT 444  
CF307749 28 bp mRNA linear EST 15-AUG-2003  
LOCUS ABF--01-E17.b1 ABF3-overexpressing transgenic rice, plasmid cDNA  
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--01-E17; mRNA sequence.  
ACCESSION CF307749  
VERSION CF307749.1 GI:33679510  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretaceae; Oryzaeae; Oryza.

REFERENCE 1 (bases 1 to 28)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..28  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone\_lib="ABF--01-E17"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH108"  
/clone\_lib="ABF3-overexpressing transgenic rice plasmid  
cDNA library (ABF)"  
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABF-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.3%; Score 20.2; DB 1; Length 28;  
Best Local Similarity 88.0%; Pred. No. 3.7e+02;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTNTTTTTTTTTTTTCTTTGCTT 4488  
Db 1 TTTTNTTTTTTTTTTTTCTTTGCTT 25

RESULT 445  
AZ836072 28 bp DNA linear GSS 20-FEB-2001  
LOCUS 2M0130K08R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
DEFINITION clone UUC2M0130K08 R, genomic survey sequence.  
ACCESSION AZ836072  
VERSION AZ836072.1 GI:13005980  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 28)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0130 row: K column: 08  
Seq primer: CACACGGAACAGCTATGACC  
Class: plasmid ends

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FEATURES
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High quality sequence stop: 28.
Location/Qualifiers
1..28
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0130K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20.2; DB 1; Length 28;
Best Local Similarity 88.0%; Pred. No. 3.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTGTCTT 4488
Db 2 TTTTTCCTTTTTCCTTTTGTCTT 26

RESULT 446
LOCUS TA29A09P 28 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA Clone 29a09, forward sequence, genomic survey sequence.
ACCESSION AL453073
VERSION AL453073.1 GI:11854584
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 28)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
DIRECT SUBMISSION
TITLE Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk
JOURNAL
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES
source
Location/Qualifiers
1..28
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="29a09"

Query Match 0.3%; Score 20.2; DB 1; Length 28;
Best Local Similarity 88.0%; Pred. No. 3.7e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTGTCTT 4488
Db 1 TTTTTCCTTTTTCCTTTTGTCTT 25

RESULT 447
LOCUS BO583967 29 bp mRNA linear EST 06-DEC-2002
DEFINITION S013297-024-004-B01-T7 MP1Z-ADIS-024-inflorescence Beta vulgaris cDNA clone 024-004-B01 3-PRIME, mRNA sequence.
ACCESSION BO583967
VERSION BO583967.1 GI:26113544
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Anaranthaceae; Beta.
REFERENCE 1 (bases 1 to 29)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M., Drugowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H. and Radloff,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 29 Std Error: 0.00
Plate: 4 row: B column: 01
Seq primer: T7; GTAATACGACTCACTATAGGCG.

FEATURES
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Location/Qualifiers
1..29
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding line)"
/db_xref="GABI:182728"
/db_xref="taxon:161934"
/clone="024-004-B01"
/tissue_type="inflorescence"
/lab_host="EMDH10B"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation:
SP6-Sali-CCACGCGTCGCG-Sprime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 20.2; DB 1; Length 29;
Best Local Similarity 88.0%; Pred. No. 4e+02;

```



```

DEFINITION AU268044 VS Dictyostelium discoideum cDNA clone VSH836 5', mRNA
sequence.
ACCESSION AU268044
VERSION AU268044.1 GI:20526842
KEYWORDS EST.
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
REFERENCE 1 (bases 1 to 31)
AUTHORS Urushihara, H., Morio, T., Saito, T., Koriki, E., Ochiai, H., Maeda, M.,
Takeuchi, I., Kohara, Y. and Tanaka, Y.
TITLE Population analysis of cDNAs from unicellular and multicellular
stages of Dictyostelium discoideum
JOURNAL Unpublished (2002)
COMMENT Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan
Tel: 81-298-53-4664
Fax: 81-298-53-6614
Email: hideko@biol.tsukuba.ac.jp.

FEATURES
source
1..31
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="VSH836"
/sex="mat A"
/dev_stage="vegetative"
/clone_lib="VS"

Query Match 0.3%; Score 20.2; DB 1; Length 31;
Best Local Similarity 88.0%; Pred. No. 4.6e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
Db 26 TTTTAAATTTTCTTTTCTTTTCTTTT 2

RESULT 451
BO591372
LOCUS BO591372 31 bp mRNA linear EST 06-DEC-2002
DEFINITION E012712-024-017-115-T7 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-017-115 3-PRIME, mRNA sequence.
ACCESSION BO591372
VERSION BO591372.1 GI:26120955
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1 (bases 1 to 31)
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stal, D., Wruck, A., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE Construction of a 'unigenes' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishnaa@mpiz-koeln.mpg.de
Insert Length: 31 Std Error: 0.00
Plate: 17 row: I column: 15
Seq primer: T7; GTAATACGACTCCTATAGGCG.
Location/Qualifiers

FEATURES
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1..31
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:188741"
/db_xref="taxon:161934"
/clone="024-017-115"
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MP1Z-ADIS-024-storage root"
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCTCCG-Sprime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Best
Project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.3%; Score 20.2; DB 1; Length 31;
Best Local Similarity 88.0%; Pred. No. 4.6e+02;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTTCTTTTCTTT 4488
Db 1 TTTTCTTTTCTTTTCTTTTCTTTTCTTT 25

RESULT 452
CF297930
LOCUS CF297930 31 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--01-B17-g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-B17, mRNA sequence.
ACCESSION CF297930
VERSION CF297930.1 GI:33669691
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1 (bases 1 to 31)
AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES
source
1..31
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--01-B17"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 20.2; DB 1; Length 31;
Best Local Similarity 88.0%; Pred. No. 4.6e+02;

```



Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTT... 4488  
 Db 31 TTTT... 7

RESULT 453  
 AZ486763  
 LOCUS  
 DEFINITION 31 bp DNA linear GSS 05-OCT-2000  
 clone UUGC1M0315A11 P, genomic survey sequence.

ACCESSION AZ486763  
 VERSION AZ486763.1 GI:10653856

KEYWORDS  
 SOURCE GSS.

ORGANISM Mus musculus (house mouse)

REFERENCE  
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 31)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT Unpublished (2000)

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0315 row: A column: 11  
 Seq primer: CTTTGTAAACGACGCCAGT  
 Class: plasmid ends

High quality sequence stop: 31.

FEATURES  
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 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20.2; DB 1; Length 31;  
 Best Local Similarity 88.0%; Pred. No. 4.6e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTT... 4488  
 Db 1 TTTT... 25

RESULT 454

AZ785111

LOCUS

DEFINITION 31 bp DNA linear GSS 16-FEB-2001

clone UUGC2M0028B14 R, genomic survey sequence.

ACCESSION AZ785111

VERSION AZ785111.1 GI:12921525

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 31)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

JOURNAL  
 COMMENT Unpublished (2000)

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunne@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0028 row: B column: 14  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends

High quality sequence stop: 31.

FEATURES  
 Location/Qualifiers

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 /sex="Male"

/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20.2; DB 1; Length 31;  
 Best Local Similarity 88.0%; Pred. No. 4.6e+02;  
 Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;





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Best Local Similarity 100.0%; Pred. No. 1.8e+02; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 4464 TTTT... 4483
Db 1 TTTT... 20

RESULT 461
CF302027 20 bp mRNA linear EST 15-AUG-2003
DEFINITION 7LEAF--07-C16.bi Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--07-C16, mRNA sequence.
ACCESSION CF302027
VERSION CF302027.1 GI:33673788
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..20
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-C16"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/notes="vector: PCR4-TOPO; Site_1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 462
CF310604/c 20 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--05-F14.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--05-F14, mRNA sequence.
ACCESSION CF310604
VERSION CF310604.1 GI:33682365
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

```

```

TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..20
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/dev_stage="14 days after germination"
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/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: PCR4-TOPO; Site_1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT... 4483
Db 20 TTTT... 1

RESULT 463
CF313067/c 20 bp mRNA linear EST 15-AUG-2003
LOCUS HD--01-B02.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--01-B02, mRNA sequence.
ACCESSION CF313067
VERSION CF313067.1 GI:33684828
KEYWORDS EST.
SOURCE
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 20)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..20
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HD--01-B02"
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/lab_host="E.coli DH10B"
/clone_lib="OshDAC1-overexpressing transgenic rice plasmid
cDNA library (HD)"

```







**AUTHORS**  
 Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B., Chissee, S., Dietrich, N., Dubuque, T., Pavello, A., Gish, W., Hawkins, M., Huleman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Maira, M.

**TITLE**  
 Generation and analysis of 280,000 human expressed sequence tags

**JOURNAL**  
 MEDLINE  
 97044478

**PUBMED**  
 8889549

**COMMENT**  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 Source: IMAGE Consortium, LNL  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Seq primer: M13RPI  
 High quality sequence stop: 21.

**FEATURES**  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:77095"  
 /sex="Female"  
 /dev\_stage="49 year old"  
 /lab\_host="SOLR cells (kanamycin resistant)"  
 /clone\_lib="Stratagene ovary (#937217)"  
 /note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; ~5' adaptor sequence: 5' GAATTCGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTATTTTATTTT 3'."

**Query Match**  
 Best Local Similarity 100.0%; Score 20; DB 1; Length 20;  
 Pred. No. 1.8e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Cy**  
 4464 TTTTATTTTATTTTATTTT 4483  
 1 TTTTATTTTATTTTATTTT 20

**Db**  
 1 TTTTATTTTATTTTATTTT 20

**RESULT 473**  
 AZ307671 20 bp DNA linear GSS 29-SEP-2000  
 LOCUS 1M0009M20R Mouse 10kb plasmid UUCGM library Mus musculus genomic  
 DEFINITION clone UUCGM0009M20 R, genomic survey sequence.  
 ACCESSION AZ307671  
 VERSION AZ307671.1 GI:10346897  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0009 row: M column: 20  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.

**FEATURES**  
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 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUCGM0009M20"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCGM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMW42 (gl[4732114]pb[AF129072.1]), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**Query Match**  
 Best Local Similarity 100.0%; Score 20; DB 1; Length 20;  
 Pred. No. 1.8e+02; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Cy**  
 4464 TTTTATTTTATTTTATTTT 4483  
 1 TTTTATTTTATTTTATTTT 20

**Db**  
 1 TTTTATTTTATTTTATTTT 20

**RESULT 474**  
 AZ333980 20 bp DNA linear GSS 29-SEP-2000  
 LOCUS 1M0063K10F Mouse 10kb plasmid UUCGM library Mus musculus genomic  
 DEFINITION clone UUCGM0063K10 F, genomic survey sequence.  
 ACCESSION AZ333980  
 VERSION AZ333980.1 GI:10400856  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Irlam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA





Email: ddunn@genetics.wash.edu  
Insert length: 10000      Std Error: 0.00  
Plate: 0076      row: F      column: 13  
Seq primer: CGTTGTAAACGACGCGCCAGT  
Class: plasmid ends  
High quality sequence step: 20.

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musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PMD2 (gii1473111|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match	0.3%	Score 20	DB 1	Length 20
Best Local Similarity	100.0%	Pred. No.	1.8e+02	
Matches	20	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0
QY	4464	TTTTTTTTTTTTTTTTTTTT	4483	
Db	20	TTTTTTTTTTTTTTTTTTTT	1	

RESULT 477	LOCUS	DEFINITION
AZ345856	AZ345856	20 bp DNA linear
	1M0080617R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0080617 R, genomic survey sequence.	GSS 29-SEP-2000

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 20)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Relliy, M., Rose, M., Rose, R., Stokes, R., Tingley, A., von Niederhausern, A. and Wright, D. Weis, R.	Mouse whole genome scaffolding with paired end reads from 10kbp

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Plate: 0080 row: G column: 17
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Class: plasmid ends
High quality sequence stop: 20.
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/clone_lib="Mouse 10kb plasmid UGGCM library"
/notes="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse Resource
http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
sheared DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PMD2 [g14732119|g1473207.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptor complementary to the insert adaptors and
purified. The sheared, adaptor mouse DNA was annealed to
adaptor vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

```

```
Query Match      0.3%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT	478				
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REFERENCE	1 (bases to 20)
AUTHORS	
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,	
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T.,	
Relly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von	
Niederhausen, A. and Wright, D. Weiss, R.	
TITLE	
Mouse whole genome scaffolding with paired end reads from 10kx	

Plate: 0089 row: B column: 18  
 Seq primer: CGTTGTAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

## FEATURES

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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
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Query Match 0.3%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483  
 Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

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 ACCESSION A2357623  
 VERSION A2357623.1 GI:10471335  
 KEYWORDS GSS.

## SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiser, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiser

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0099 row: A column: 20

## JOURNAL COMMENT

Unpublished (2000)

Contact: Robert B. Weiser

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Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0099 row: A column: 20

Seq primer: CGTTGTAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 20.  
 Location/Qualifiers

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Query Match 0.3%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 20 TTTT TTTT TTTT TTTT TTTT TTTT 1

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 LOCUS  
 DEFINITION 1M0120024F Mouse 10kb plasmid UUCG1M library Mus musculus genomic clone UUCG1M0120024 F, genomic survey sequence.  
 ACCESSION A2369734  
 VERSION A2369734.1 GI:10483434  
 KEYWORDS GSS.

## SOURCE

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiser, R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiser

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0120 row: O column: 24

Seq primer: CGTTGTAACGACGCCAGT

## JOURNAL COMMENT

Unpublished (2000)

Contact: Robert B. Weiser

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Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0120 row: O column: 24

Seq primer: CGTTGTAACGACGCCAGT

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Location/Qualifiers  
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/clone\_1lb="Mouse 10kb plasmid UUCGM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4464 TTTTTTTTTTTTTTTTTT 4483  
Db 20 TTTTTTTTTTTTTTTTTT 1

RESULT 481  
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DEFINITION IM0145C1R Mouse 10kb plasmid UUCGM library Mus musculus genomic  
clone UUCGM0145C11 R, genomic survey sequence.  
ACCESSION  
AZ386573  
VERSION  
AZ386573.1 GI:10500273  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,  
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0145 row: C column: 11  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

JOURNAL  
COMMENT

Class: plasmid ends  
High quality sequence stop: 20.  
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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UUCGM library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 20 TTTTTTTTTTTTTTTTTT 1

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ACCESSION  
AZ396481  
VERSION  
AZ396481.1 GI:10511553  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,  
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0161 row: K column: 02  
Seq primer: CGTTGTAAACGACGGCCAGCT  
Class: plasmid ends  
High quality sequence stop: 20.

JOURNAL  
COMMENT





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/strain="C57BL/6J"
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Db 20 TTTTTTTTTTTTTTTTTT 1

RESULT 491				
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LOCUS				
DEFINITION	AZ588011	20 bp	DNA	linear
DESCRIPTION	IM0396A13 Mouse 10kb plasmid UUC1M library Mus musculus genomic clone UUC1M0396A13 F, genomic survey sequence.			

RESULT	492
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LOCUS	20 bp DNA linear
DEFINITION	IM0429A14R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
ACCESSION	clone UUGCG1M0429A14 R, genomic survey sequence.
	AZ607328

ACCESSION	AZ588011
VERSION	AZ588011.1
KEYWORDS	GSS.

VERSION	AZ607328.1	GI:11729518
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	

ORGANISM	REFERENCE
<i>B. musculus</i>	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus	
1 (Passes 1 to 20)	
Dunn, D., Acyag, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,	

ORGANISM	REFERENCE
<i>Mus musculus</i>	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, S., Meenen, E., Pedersen, T.,
<i>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</i>	
<i>Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus</i>	
<i>1 (bases 1 to 20)</i>	

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb

TITLE	Abstract	Full Text
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	Abstract	Full Text

**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss

**JOURNAL COMMENT** Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

**Tel: 801 585 5606**  
**Fax: 801 585 7177**

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00

Plate: 0396 row: A column: 13  
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Class: plasmid ends  
High quality sequence stop: 20.

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/mol_type="genomic DNA"
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lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"

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clone 11="Mouse 10kb plasmid UNGCM library"  
musculus C57BL/6J (male). Purified genomic DNA from M.  
Laboratory Mouse DNA Resource  
<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 [gi|473214|gb|AF12072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match	0.34;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 1.8e+02;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

RESULT	492
AZ607328/c	
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DEFINITION	20 bp DNA linear GSS 13-DEC-2000
	1M0429A1R Mouse 10kb genomic U06C1M library Mus musculus genomic
	clone U06C1M0429A1 R, genomic survey sequence.

LOCUS	20 bp	DNA	line
DEFINITION	AZ607328	1M0429A14R	Mouse 10kb plasmid UUGC1M library Mu
		clone UUGC1M0429A14 R,	genomic survey sequence.

VERSION	AZ607328.1	GI:11729518
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	

**SOURCE** Mus musculus (house mouse)

REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

REFERENCE  
AUTHORS  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., H  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen

TITLE	DESCRIPTION
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts	

**COMMENT**  
Contact: Robert B. Weiss  
University of Utah Genome Center

84112, USA  
Tel: 801 585 5606

Fax: 801 585 7177  
Email: [ddunn@gene](mailto:ddunn@gene)

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Insert Length: 10000      Std Error: 0.0000
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Class: plasmid ends

High quality sequence stop: 20  
Location/Qualifiers

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/clone_libs="Mouse 10kb plasmid UTGCM library"

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/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||  
Db 20 TTTTTTTTTTTTTTTTTT 1

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LOCUS 1M0460K05R Mouse 10kb plasmid UUCG1M library Mus musculus genomic  
DEFINITION clone UUCG1M0460K05 R, genomic survey sequence.

ACCESSION AZ623155  
VERSION AZ623155.1 GI:11745345  
KEYWORDS GSS.

SOURCE Mus musculus  
ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
JOURNAL Unpublished (2000)

COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0460 row: K column: 05  
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Class: plasmid ends

High quality sequence stop: 20.  
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/clone\_lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g114732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TTTTTTTTTTTTTTTTTT 20

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DEFINITION clone UUCG1M0460L12 R, genomic survey sequence.

ACCESSION AZ623214  
VERSION AZ623214.1 GI:11745404  
KEYWORDS GSS.

SOURCE Mus musculus  
ORGANISM Mus musculus (house mouse)

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausen,A. and Wright,D.,Weise,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)

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University of Utah Genome Center

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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
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Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends

High quality sequence stop: 20.  
Location/Qualifiers

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/clone\_lib="Mouse 10kb plasmid UUCG1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson

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1..20
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/sex="Male"
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/clone_lib="E. coli plasmid 10kb UUGC1M library"
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Laboratory Mouse DNA Resource

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/lab_host="B. Coli strain XL10-Gold, T1-resistant, F-
/clone.lib="Mouses 10kb plasmid UGGCM library"
/notes="Vector: pMD4.6; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
http://www.jax.org/resources/documents/dnares/". The DNA

```

was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483  
Db 1 TTTTTTTTTTTTTTTTTT 20

RESULT 497  
AZ650271/c 20 bp DNA linear GSS 14-DEC-2000  
LOCUS  
DEFINITION IM0520C21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0520C21 F, genomic survey sequence.

ACCESSION  
AZ650271  
A2650271.1 GI:11764588

VERSION  
GSS.

KEYWORDS  
Mus musculus (house mouse)

SOURCE  
Mus musculus

ORGANISM  
Mus musculus

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS  
1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

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84112, USA

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0520 row: C column: 21

Seq primer: CGTGTAAACAGACGCCAGC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

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/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0520C21"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483  
Db 20 TTTTTTTTTTTTTTTTTT 1

RESULT 498  
AZ760838/c 20 bp DNA linear GSS 16-FEB-2001  
LOCUS  
DEFINITION IM0554A24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0554A24 R, genomic survey sequence.

ACCESSION  
AZ760838  
A2760838.1 GI:12869112

VERSION  
GSS.

KEYWORDS  
Mus musculus (house mouse)

SOURCE  
Mus musculus

ORGANISM  
Mus musculus

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS  
1 (bases 1 to 20)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D., Weis, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

Unpublished (2000)

CONTACT: Robert B. Weiss

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0554 row: A column: 24

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

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/strain="C57BL/6J"

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/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: pMD42nv, Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a

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1. 20
/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGCM0560M02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGGCM library"
/notes="Vector: pMD249; Purified genomic DNA from C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4

```

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UGGCM0562H04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_id="Mouse 10kb plasmid UGGCM library"
/notes="Vector: pMD42nyv, Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were

```











adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 509  
AZ809306/c 20 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION 2M0073D15f Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0073D15 F, genomic survey sequence.

ACCESSION  
AZ809306  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

JOURNAL  
COMMENT  
TITLE  
AUTHORS  
REFERENCE

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Tel: 801 585 5606  
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Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0073 row: D column: 15  
Seq primer: CATTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
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Location/Qualifiers

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/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into

chemically-competent *E. coli* XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 510  
AZ810986/c 20 bp DNA linear GSS 20-FEB-2001  
LOCUS  
DEFINITION 2M0076I20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M0076I20 R, genomic survey sequence.

ACCESSION  
AZ810986  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 20)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

JOURNAL  
COMMENT  
TITLE  
AUTHORS  
REFERENCE

Contact: Robert B. Weiss  
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Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0076 row: I column: 20  
Seq primer: CACACAGGAACGATATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

FEATURES  
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Location/Qualifiers

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/clone="UUGC2M0076I20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into

and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT 4483  
TTTT TTTT TTTT TTTT TTTT 1

Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 511  
AZ813908/c

LOCUS

DEFINITION 20 bp DNA linear GSS 20-FEB-2001  
2M00812F1F2 Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0081 row: F column: 21

Seq primer: CGTGTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. 20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC2M0081F21"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT 4483  
TTTT TTTT TTTT TTTT TTTT 1

Db 20 TTTT TTTT TTTT TTTT TTTT 1

RESULT 512  
AZ817323/c

LOCUS

DEFINITION 20 bp DNA linear GSS 20-FEB-2001  
2M0086C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

University of Utah Genome Center

University of Utah

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0086 row: F column: 20

Seq primer: CACACAGGAAACACGCTATGACC

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. 20

/organism="Mus musculus"

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/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (g14732114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match	0.3%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1	6e+02;	
Matches	20;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Qx	4464	TTTTTTTTTTTTTTTTTTTT	4483	
Db	20	TTTTTTTTTTTTTTTTTTTT	1	

RESULT 513					
LOCUS	AZ817414/C				
DEFINITION	AZ817414	20 bp	DNA	linear	GSS 20-FEB-2001
ACCESSION	200008608R	Mouse 10kb	plasmid	UUCiM library	Mus musculus genomic
VERSION	clone UUCG2M0086X08 R,				genomic survey sequence.
KEYWORDS	AZ817414				
SOURCE	AZ817414.1	GI:12987238			
ORGANISM	GSS.				
	Mus musculus (house mouse)				
	Mus musculus				
	Eukaryota; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 20)				
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C., Ismail,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellay,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.				
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb				
JOURNAL	Plasmid inserts				
COMMENT	Unpublished (2000)				
	Contact: Robert B. Weiss				

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84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)  
Insert Length: 1000 Std Error: 0.00  
Plate: 0086 row: K column: 08  
Seq primer: CACACGGAACACTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.

## FEATURES

### source

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/organism="Mus musculus"
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/strain="C57BL/6J"
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/clone="U08C2M0086K08"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/clone.lib="Mouse 10kb plasmid U08C1M library"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

	Best Local Similarity	100.0%	Pred. No.	1.8e+02;	Indels	0;	Gaps	0;
Oy	Matches	20	Conservative	0;	Mismatches	0;		
		4464	TTTTTTTTTTTTTTTTTT	4463				
Db		20	TTTTTTTTTTTTTTTTTTT	1				

RESULT 514	
AZ817467/c	
LOCUS	AZ817467
DEFINITION	20 bp DNA linear GSS 20-FEB-2001
ACCESSION	AZ817467
VERSION	AZ817467
KEYWORDS	clone UUC2M0086j15 R, genomic survey sequence.
SOURCE	AZ817467.1 GI:12987291
ORGANISM	GSS.
	Mus musculus (house mouse)
	Mus musculus

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 20)	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellay, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.	Mouse whole genome scaffolding with paired end reads from 10kb

**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel.: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0086 row: J column: 15  
Seq primer: CACACAGAAACACACTGAC  
Class: plasmid ends  
High quality sequence stop: 20.

## FEATURES

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Prid No. 1.8e+02;

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/clone\_lid="Mouse 10kb plasmid U08220 library"  
/note="Vector: pMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (g14732114[gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptor complementary to the insert adaptor and  
purified. The sheared and adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

[illegible]

RESULT 51.5  
A7817E08

LOCUS	AZ817608	20 bp	DNA	linear	GSS 20-FEB-2001
DEFINITION	2M0087K08F	Mouse 10kb	plasmid	U9C1M library	Mus musculus genomic
DESCRIPTION	clone U9CGCM0087K08 F,	genomic	survey	sequence.	

ACCESSION	AZ817608
VERSION	AZ817608.1
	GI:12987516

SOURCE ORGANISM	Mus musculus (house mouse) Mus musculus
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99	99
100	100

## REFERENCE AUTHORS

TITLE	DESCRIPTION
Mouse whole genome scaffolding with paired end reads from 10kb	

**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLc, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0087 row: k column: 08  
Seq primer: CGTGTAAATCAGCGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.

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 /db\_xref="taxon:10090"  
 /clone="U08C2M0087K08"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid U08C1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (<http://www.jax.org/resources/documents/dnares/>). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivatived  
 of pMD2 (gill1473111[gbl]AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match	0.3%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1.8e+02;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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Oy      4464 TTTTTTTTTTTTTTTT 4483  
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Db      1 TTTTTTTTTTTTTTTT 20
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RESULT 516

LOCUS	AZ818489	20 bp	DNA	linear	GSS 20-FEB-2001
DEFINITION	2M0088K01 Mouse 10kb plasmid UGCLM library Mus musculus genomic				
FEATURES	clone UUGC2M0088K01 R, genomic survey sequence.				

ACCESSION	AZ818489
VERSION	AZ818489.1
	GI:12988397

SOURCE Mus musculus (house mouse).

## REFERENCE

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausen, A. and Wright, D., Weiss, R.

**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel.: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0088 row: K column: 01  
 Seq primer: CACACAGGAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.

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organism="Mus musculus"  
mol\_type="genomic DNA"  
strain="C57BL/6J"  
db\_xref="taxon:10090"  
clone="U082M0088K01"  
sex="Male"  
lab\_host="E. Coli strain XL10-Gold, Ti-resistant, F-"  
clone\_lib="mouse 10kb plasmid UGCGM library"  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD2 (g14732114[g]/AF12972.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptorized mouse DNA was annealed to  
adaptorized vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match	0.3%	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%	Pred. No. 1.8e+02;		
Matches 20; Conservative	0;	Mismatches	0;	Indels 0
				Gaps 0

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483  
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 Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 517  
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 LOCUS  
 DEFINITION 2M0132K13R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 clone UGCG2M0132K13 R, genomic survey sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 ORGANISM  
 SOURCE  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
 Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weis,R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0083 row: M column: 05  
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 Class: plasmid ends  
 High quality sequence stop: 20.

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 /db\_xref="taxon:10090"  
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 /clone\_lib="Mouse 10kb plasmid UGCG1M library"  
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 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g1473214|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483

Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 518  
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 LOCUS  
 DEFINITION 2M0132K13R Mouse 10kb plasmid UGCG1M library Mus musculus genomic  
 clone UGCG2M0132K13 R, genomic survey sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 ORGANISM  
 SOURCE  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,  
 Relliy,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weis,R.

TITLE  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weis  
 University of Utah Genome Center  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0132 row: K column: 13  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 20.

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 /db\_xref="taxon:10090"  
 /clone="UGCG2M0132K13"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCG1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g1473214|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4483

Db : 20 TTTTTTTTTTTTTTTTTT

RESULT 519	LOCUS	DEFINITION	ACCION
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		200139H16 Mouse 10kb plasmid UUCG1M library Mus musculus genomic	
		clone UUCG2M0139H16 F, genomic survey sequence.	
		20041342	

SOURCE ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

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Query Match Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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|||||
Db 20 TTTTYYYYTTTTTTTTTTTT 1
|||||

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RESULT	520	
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LOCUS		
DEFINITION	20 bp DNA linear	GSS 20-FEB-2001
ACCESION	AZ841558	
	2M0133A10R Mouse 10kb plasmid UUC1M library Mus musculus genomic	
	clone UUCG2M0133A10 R, genomic survey sequence.	
	17601550	

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	unpublished (2000)
	Contact: Robert B. Weiss
	weiss@genome.wustl.edu

Query Match	0.34;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.04;	Pred. No. 1.8e+02;		
Matches	20;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Oy	4464	TTTTTTTTTTTTTTTTTTTT	4463	
Db	1	TTTTTTTTTTTTTTTTTTTT	20	

RESULT 521  
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 DEFINITION 2M0165003F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0165003 F, genomic survey sequence.  
 ACCESSION  
 AZ858052  
 VERSION  
 AZ858052.1 GI:13050813  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 REFERENCE  
 Authors  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausen, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE  
 Unpublished (2000)  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 /sex="Male"  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g14732114[gb|AF129072.1]) a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483  
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RESULT 522  
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 LOCUS 20 bp DNA linear GSS 26-APR-2001  
 DEFINITION 2M0193G23R Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
 clone UUGC2M0193G23 R, genomic survey sequence.  
 ACCESSION  
 AZ936914  
 VERSION  
 AZ936914.1 GI:13795495  
 KEYWORDS  
 GSS.  
 SOURCE  
 Mus musculus (house mouse)  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 REFERENCE  
 Authors  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausen, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 TITLE  
 Unpublished (2000)  
 JOURNAL  
 COMMENT  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0193 row: 0 column: 23  
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 /sex="Female"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC2M library"  
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 musculus C57BL/6J (female) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g14732114[gb|AF129072.1]) a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483  
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RESULT 523



AZ949180  
 LOCUS 20 bp DNA linear GSS 27-APR-2001  
 DEFINITION 2M0212102R Mouse 10kb plasmid UNGC2M library Mus musculus genomic  
 clone UNGC2M0212102 R, genomic survey sequence.  
 ACCESSION AZ949180  
 VERSION 1  
 KEYWORDS GI:13820407  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464  
 1  
 4483

RESULT 524  
 AZ963973

LOCUS 20 bp DNA linear GSS 27-APR-2001  
 DEFINITION 2M023301F Mouse 10kb plasmid UNGC2M library Mus musculus genomic  
 clone UNGC2M023301 F, genomic survey sequence.  
 ACCESSION AZ963973  
 VERSION 1  
 KEYWORDS GI:13835200  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 20)  
 Dumm,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 JOURNAL Contact: Robert B. Weiss  
 COMMENT University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0233 row: 1 column: 01  
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 High quality sequence stop: 20.  
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 /clone\_1lb="Mouse 10kb plasmid UNGC2M library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4464  
 1  
 4483

RESULT 525  
 AL048777/c

AL048777

21 bp

mRNA

linear

EST 04-SEP-2003

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DEFINITION DKF2P566N053_r1 566 (synonym: hfk42) Homo sapiens cDNA clone
ACCESSION DKF2P566N053, mRNA sequence.
VERSION AL048777
KEYWORDS EST, 4727848
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 21)
JOURNAL Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
COMMENT Unpublished (1999)
CONTACT: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES
SOURCE
location/Qualifiers
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/clone_lib="566 (synonym: hfk42)"
/notes="Vector: pAMP1, Site_1: NotI; Site_2: SalI"

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 21 TTTT TTTT TTTT TTTT TTTT 2

RESULT 526 21 bp mRNA linear EST 10-OCT-2003
BX556006 Glossina morsitans morsitans adult infected gut Glossina
LOCUS morsitans morsitans cDNA clone tse24c09_p1c, mRNA sequence.
DEFINITION
ACCESSION BX556006
VERSION BX556006.1 GI:33379965
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AUTHORS Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
TITLE 1 (bases 1 to 21)
JOURNAL Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
COMMENT Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
MIPS Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
MIPS Genome Biol. 4 (10), R63 (2003)

JOURNAL 22881942
MEDLINE 14519198
PUBMED
CONTACT: Hall N
SOURCE Pathogen Sequencing Unit
COMMENT The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

FEATURES
SOURCE
location/Qualifiers
1..21
/organism="Glossina morsitans morsitans"
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/db_xref="taxon:37546"
/clone="tse24c09_p1c"
/tissue_type="adult infected gut"
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gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 20; DB 1; Length 21;
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4485
Db 21 TTTT TTTT TTTT TTTT TTTT 2

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DEFINITION DKF2P566N053_r1 566 (synonym: hfk42) Homo sapiens cDNA clone
ACCESSION DKF2P566N053, mRNA sequence.
VERSION AL048777
KEYWORDS EST, 4727848
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 21)
JOURNAL Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.
COMMENT Unpublished (1999)
CONTACT: MIPS
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4464 TTTT TTTT TTTT TTTT TTTT 4483
Db 21 TTTT TTTT TTTT TTTT TTTT 2

RESULT 527 21 bp mRNA linear EST 10-OCT-2003
BX558161 Glossina morsitans morsitans adult infected gut Glossina
LOCUS morsitans morsitans cDNA clone tse37a05_p1c, mRNA sequence.
DEFINITION
ACCESSION BX558161
VERSION BX558161.1 GI:33429302
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
AUTHORS Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
TITLE 1 (bases 1 to 21)
JOURNAL Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
COMMENT Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
MIPS Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
MIPS Genome Biol. 4 (10), R63 (2003)

JOURNAL 22881942
MEDLINE 14519198
PUBMED
CONTACT: Hall N
SOURCE Pathogen Sequencing Unit
COMMENT The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW

FEATURES
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location/Qualifiers
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/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
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/clone="tse37a05_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match 0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 4466 TTTT TTTT TTTT TTTT TTTT 4485
Db 21 TTTT TTTT TTTT TTTT TTTT 2

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Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
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 Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 531  
 CF295642  
 LOCUS 21 bp mRNA linear EST 14-AUG-2003  
 DEFINITION sativa cDNA clone 30DGS--05-K20, mRNA sequence.  
 ACCESSION CF295642  
 VERSION CF295642.1 GI:33664675  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 21)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /tissue\_type="leaf"  
 /dev\_stage="30 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
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 RT-PCR."

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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 TTTT TTTT TTTT TTTT TTTT 20

RESULT 532  
 CF297615  
 LOCUS 21 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 30DGS--08-J10.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 sativa cDNA clone 30DGS--08-J10, mRNA sequence.  
 ACCESSION CF297615  
 VERSION CF297615.1 GI:33666648  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 21)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

Query Match 0.3%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
 |||||  
 Db 1 TTTT TTTT TTTT TTTT TTTT 20

COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1..21  
 /organism="Oryza sativa"  
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 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
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 /clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 21;  
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
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 Db 21 TTTT TTTT TTTT TTTT TTTT 2

RESULT 533  
 CF298322  
 LOCUS 21 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--01-K14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--01-K14, mRNA sequence.  
 ACCESSION CF298322  
 VERSION CF298322.1 GI:33670083  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 21)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,Y.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 /cultivar="Nackdong"  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 21;  
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
 |||||  
 Db 21 TTTT TTTT TTTT TTTT TTTT 2

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
 |||||  
 1 TTTT TTTT TTTT TTTT 20

RESULT 534  
 CF300809  
 LOCUS 7LEAF--05-G20.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION  
 ACCESSION CF300809  
 VERSION CF300809.1 GI:33672570  
 KEYWORDS EST  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 21)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
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 1 TTTT TTTT TTTT TTTT 20

RESULT 535  
 CF312715  
 LOCUS ABF--08-J10.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (ABF) Oryza sativa cDNA clone ABF--08-J10, mRNA sequence.  
 ACCESSION CF312715  
 VERSION CF312715.1 GI:33684476  
 KEYWORDS EST  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 21)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
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 line."

Query Match 0.3%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4483  
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 21 TTTT TTTT TTTT TTTT 2

RESULT 536  
 CF316073  
 LOCUS HD--05-D16.b1 OshDACL1-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (HD) Oryza sativa cDNA clone HD--05-D16, mRNA sequence.  
 ACCESSION CF316073  
 VERSION CF316073.1 GI:33687834  
 KEYWORDS EST  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 21)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
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Query Match 0.3%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483  
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 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 540  
 CF338057/c  
 LOCUS  
 DEFINITION JMT--08-M03.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--08-M03, mRNA sequence.  
 CF338057  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

CF338057.1 GI:33824485  
 EST.  
 Oryza sativa  
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaeae; Oryza.  
 1. (bases 1 to 21)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 321 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
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 /organism="Oryza sativa"  
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 prepared from Arabidopsis Jasmonate Carboxyl  
 methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483  
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 Db 21 TTTT TTTT TTTT TTTT TTTT TTTT 2

RESULT 541  
 CF338522  
 LOCUS  
 DEFINITION RCL1--01-P04.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 Oryza sativa cDNA clone RCL1--01-P04, mRNA sequence.

CF338522  
 LOCUS  
 DEFINITION RCL1--01-P04.g1 Regenerated callus lambda phage cDNA library (RCL1)  
 Oryza sativa cDNA clone RCL1--01-P04, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

CF338522  
 EST.  
 Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaeae; Oryza.  
 1. (bases 1 to 21)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 321 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

FEATURES  
 source  
 1..21  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
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 /tissue\_type="callus"  
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 /lab\_host="E.coli SOLR"  
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 (RCL1)"  
 /note="vector: pBluescript SK(+); Site 1: SstI; Site 2:  
 XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
 end with SstI and 3' end with XhoI site. Callus was  
 induced on 2N6 media for 30 days and cultured for 36hrs on  
 regenerated media"

Query Match 0.3%; Score 20; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483  
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 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 542  
 AZ348593/c

LOCUS  
 DEFINITION 1M0085A13F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0085A13 F, genomic survey sequence.  
 AZ348593  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AZ348593  
 1M0085A13F Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0085A13 F, genomic survey sequence.  
 AZ348593  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

REFERENCE  
 AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1. (bases 1 to 21)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606

TITLE  
 JOURNAL  
 COMMENT







```

Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTNTTTTTTTTTTTTTTTT 4483
Db 21 TTTTNTTTTTTTTTTTTTTTT 2

RESULT 547
AZ389687/c
LOCUS
DEFINITION
1M0150B10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0150B10 R, genomic survey sequence.
ACCESSION
AZ389687
VERSION
AZ389687.1 GI:10503395
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0150 row: B column: 10
Seq primer: CACACAGGAACGCTATGACC

Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0150B10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTTNTTTTTTTTTTTTTTTT 4483
Db 21 TTTTNTTTTTTTTTTTTTTTT 2

RESULT 548
AZ406936
LOCUS
DEFINITION
1M0176B24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0176B24 F, genomic survey sequence.
ACCESSION
AZ406936
VERSION
AZ406936.1 GI:10530949
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0176 row: E column: 24
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends

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High quality sequence stop: 21.
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        /strain="C57BL/6J"
        /db_xref="taxon:10090"
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        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (G114732114|GB|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
      Query Match          0.3%; Score 20; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred. No. 2e+02;
      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
      |||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 549
AZ412739
LOCUS
DEFINITION
  1M0186D23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0186D23 F, genomic survey sequence.
ACCESSION
  AZ412739
VERSION
  AZ412739.1 GI:10536752
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
  1 (bases 1 to 21)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0186 row: D column: 23
  Seq primer: CGTGTAAACGACGCCAGT
  Class: plasmid ends
  High quality sequence stop: 21.
  Location/Qualifiers

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        /strain="C57BL/6J"
        /db_xref="taxon:10090"
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        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnates/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (G114732114|GB|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
      Query Match          0.3%; Score 20; DB 1; Length 21;
      Best Local Similarity 100.0%; Pred. No. 2e+02;
      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
      |||||
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 20

RESULT 550
AZ412931
LOCUS
DEFINITION
  1M0186N08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0186N08 R, genomic survey sequence.
ACCESSION
  AZ412931
VERSION
  AZ412931.1 GI:10536944
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 21)
  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
  Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
  Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
  Niederhausern, A. and Wright, D., Weiss, R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
  Contact: Robert B. Weiss
  University of Utah Genome Center
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0186 row: N column: 08
  Seq primer: CACACAGGAACAGCTATGACC
  Class: plasmid ends
  High quality sequence stop: 21.
  Location/Qualifiers

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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```

Query Match      0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483
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Db 20 TTTTTTTTTTTTTTTTTT 1

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RESULT 553
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LOCUS      21 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0276F07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0276F07 F, genomic survey sequence.

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ACCESSION  AZ465890
VERSION     AZ465890.1 GI:10624015
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

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ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE   1 (bases 1 to 21)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts

```

```

JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center

```

```

            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177

```

```

            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00

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            Plate: 0276 row: F column: 07
            Seq primer: CGTTGTAACACGCGCCAGT

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            Class: plasmid ends
            High quality sequence stop: 21.

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FEATURES    Location/Qualifiers
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            /mol_type="genomic DNA"

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/db_xref="taxon:10090"
/clone="UUGC1M0276F07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483
      |||||
Db 1 TTTTTTTTTTTTTTTTTT 20

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RESULT 554
AZ611116/c
LOCUS

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DEFINITION  AZ611116
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            clone UUGC1M0436N02 R, genomic survey sequence.

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ACCESSION  AZ611116
VERSION     AZ611116.1 GI:11733306
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

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ORGANISM    Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE   1 (bases 1 to 21)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.

```

```

TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts

```

```

JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center

```

```

            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177

```

```

            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00

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            Plate: 0436 row: N column: 02
            Seq primer: CACACAGGAAACAGCATGACC

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            Class: plasmid ends
            High quality sequence stop: 21.

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FEATURES    Location/Qualifiers
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            /mol_type="genomic DNA"

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FEATURES
source
1. .21
Location/Qualifiers
/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="UUGC1M0564011"
/sex="Male"
/lab_host="E. Coli strain"
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/notes="Vector: PWD42nv;
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0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match      0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
      ||||| ||||| ||||| ||||| ||||| |||||
Db 21 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2

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RESULT 565
AZ815424/c
LOCUS      21 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0083H1R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0083H1 R, genomic survey sequence.
ACCESSION  AZ815424
VERSION     AZ815424.1  GI:12985332
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

```

```

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weisse,R.

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JOURNAL
Unpublished (2000)
COMMENT
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0083 row: H column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

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FEATURES
Location/Qualifiers
1..21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0083H11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

```

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%; Score 20; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
      ||||| ||||| ||||| ||||| ||||| |||||
Db 21 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 2

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RESULT 566
AZ819181/c
LOCUS      21 bp      DNA      linear      GSS 20-FEB-2001
DEFINITION 2M0089110R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0089110 R, genomic survey sequence.
ACCESSION  AZ819181
VERSION     AZ819181.1  GI:12989089
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)

```

```

ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE
1 (bases 1 to 21)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weisse,R.

```

Mus whole genome scaffolding with paired end reads from 10kb plasmid inserts

```

JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0089 row: I column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.

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FEATURES
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0089110"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4

```



10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWB2 [gi|473214|gb|AF129072.1|, a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

[illegible]

RESULT 570	BH000837	21 bp	DNA	linear	GSS 27-APR-2001
LOCUS	BH000837/c				
DEFINITION	2M0288020R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0288020 R, genomic survey sequence.				
ACCESSION	BH000837				
VERSION	BH000837.1	GI:13872063			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 21)				
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,				

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: <a href="mailto:ddunn@genetics.utah.edu">ddunn@genetics.utah.edu</a> Insert Length: 10000 Std Error: 0.00 Plate: 0288 row: 0 column: 20 Seq primer: CACACAGGAACAGCTATGACC Class: plasmid ends High quality sequence stop: 21. Location/Qualifiers 1. .21
FEATURES	source

sex="Female"  
lab\_hosts="E. coli strain XL10-Gold, T1-resistant, F-"  
clone\_lib="Mouse 10kb plasmid UUCG2M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (female) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(<http://www.jax.org/resources/documents/dnares/>). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel



## RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTT 4483  
 Db 1 TTTT...TTTTTTT 20

RESULT 574  
 CF332379  
 LOCUS 23 bp mRNA linear EST 18-AUG-2003  
 DEFINITION NACL--08-N21.g1 Rice callus plasmid cDNA library (NACL) Oryza sativa CDNA clone NACL--08-N21, mRNA sequence.  
 ACCESSION CF332379  
 VERSION CF332379.1 GI:33812983  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 23)  
 AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source  
 1..23  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="NACL--08-N21"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 30 days"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice callus plasmid cDNA library (NACL)"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTT 4483  
 Db 1 TTTT...TTTTTTT 20

RESULT 575  
 CF334077  
 LOCUS 23 bp mRNA linear EST 18-AUG-2003  
 DEFINITION JMT--03-D17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa CDNA clone JMT--03-D17, mRNA sequence.  
 ACCESSION CF334077  
 VERSION CF334077.1 GI:33816466  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

source  
 1..23  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="JMT--03-D17"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTTTT 4483  
 Db 3 TTTT...TTTTTTT 22

## RESULT 576

LOCUS 25 bp mRNA linear EST 02-MAR-2001  
 DEFINITION AU587718 BP Chicken Brain Library Gallus gallus cDNA clone ROS061C02, mRNA sequence.  
 ACCESSION AU587718  
 VERSION AU587718.1 GI:13192752  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

## REFERENCE

AUTHORS Murray,F.  
 TITLE BP Chicken Brain Library  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Frazer Murray  
 Dept. Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UK  
 Tel: +44 (0)131 527 4200  
 Fax: +44 (0)131 440 0434  
 Email: frazer.murray@bbsrc.ac.uk

GGGGCGCTTTT...TTTTTTT 3' Poly A RNA purchased from Clontech (#6854-)

## Seq primer: M13F.

Location/Qualifiers  
 1..25  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="ROS061C02"  
 /tissue\_type="Brain"  
 /dev\_stage="Unknown"

/lab\_host="DH10B"  
 /clone\_lib="BP Chicken Brain Library"  
 /note="vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned  
 unidirectionally. Primer: Oligo dr. 5' adaptor sequence:  
 5' TCAGACCTCGAG 3'; 3' adaptor sequence: 5'  
 GCGCGCGCTTTTTTTTTTTT 3' Poly A RNA purchased from  
 Clontech (\*6854-1)"

Query Match 0.3%; Score 20; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4465 TTTTTTTTTTTTTTTTTT 4484  
 |||||||  
 Db 2 TTTTTTTTTTTTTTTTTT 21

RESULT 577  
 CF310471 25 bp mRNA linear EST 15-AUG-2003  
 LOCUS  
 DEFINITION ABF--05-C07.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 library (ABF) Oryza sativa cDNA clone ABF--05-C07, mRNA sequence.  
 CF310471  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 25)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 TITLE  
 JOURNAL  
 COMMENT  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Yeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source

1..25  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="ABF--05-C07"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"  
 /note="vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 0.3%; Score 20; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483  
 |||||||  
 Db 6 TTTTTTTTTTTTTTTTTT 25

RESULT 578  
 N59260 25 bp mRNA linear EST 23-FEB-1996  
 LOCUS  
 DEFINITION yz82d11.e1 Soares\_multiple\_sclerosis\_2nbhmSP Homo sapiens cDNA

clone IMAGE:289557 3' similar to gb:M77693 DIAMINE  
 ACETYLTRANSFERASE (HUMAN);, mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

N59260  
 N59260.1 GI:1203150  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 25)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Matra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, P.,  
 Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

TITLE  
 JOURNAL  
 COMMENT

The WashU-Merck EST Project  
 Unpublished (1995)  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@wustl.wustl.edu  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality

Seq primer: ml3 -40 forward  
 High quality sequence stop: 1.

FEATURES  
 source

1..25  
 /organism="Homo sapiens"  
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 /db\_xref="GDB:3905397"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:289557"  
 /sex="male"  
 /tissue\_type="multiple sclerosis lesions"  
 /dev\_stage="Age 46"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares\_multiple\_sclerosis\_2nbhmSP"  
 /note="vector: pT7T3D (Pharmacia) with a modified  
 polylinker V.TYPE: phagemid; Site 1: Not I; Site 2: Eco  
 RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
 primer [5'  
 TGTTCACATCTGAAGTGGGAGCGCGCATTTTTTTTTTTTTTTT 3'],  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M.Patima Bonaldo. RNA from 4 multiple sclerosis  
 lesions from one patient was kindly provided by Dr. Kevin  
 G. Becker (NINDS/NIH). "

Query Match 0.3%; Score 20; DB 1; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483  
 |||||||  
 Db 1 TTTTTTTTTTTTTTTTTT 20

RESULT 579  
 AZ330737/c  
 LOCUS  
 DEFINITION  
 1M0056F09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0056F09 F, genomic survey sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AZ330737  
 AZ330737.1 GI:10392737  
 GSS.  
 Mus musculus (house mouse)  
 Mus musculus





University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0101 row: M column: 24  
 Seq primer: CGTTGTAACAGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 26.

## FEATURES

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1. .26  
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 /strain="C57BL/6J"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUCG1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT  
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 582  
 CF310560  
 LOCUS  
 DEFINITION  
 library (ABF) Oryza sativa cDNA clone ABF-05-E14, mRNA sequence.

ACCESSION  
 CF310560  
 VERSION  
 CF310560.1 GI:33682321  
 KEYWORDS  
 EST.  
 SOURCE  
 Oryza sativa

ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 1 (bases 1 to 27)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA

FEATURES  
 source  
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 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="JMT-02-H05"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="AtJMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis jasmonate Carboxyl  
 methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
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 QY 4465 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT  
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 583  
 CF333518  
 LOCUS  
 DEFINITION  
 JMT--02-H05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--02-H05, mRNA sequence.

ACCESSION  
 CF333518  
 VERSION  
 CF333518.1 GI:33815326  
 KEYWORDS  
 EST.  
 SOURCE  
 Oryza sativa

ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1. .27  
 /organism="Oryza sativa"  
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 /db\_xref="taxon:4530"  
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 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

## FEATURES

source

1. .27  
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 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="ABF-05-E14"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="ABF3-overexpressing transgenic rice plasmid  
 cDNA library (ABF)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried  
 for 2hrs. Oligo-capped mRNA was reverse transcribed and  
 then used for PCR. mRNA was prepared from ABA-responsive  
 element binding transcription factor 3 overexpression  
 line."

Query Match 0.3%; Score 20; DB 1; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4465 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT  
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 583  
 CF333518  
 LOCUS  
 DEFINITION  
 JMT--02-H05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--02-H05, mRNA sequence.

ACCESSION  
 CF333518  
 VERSION  
 CF333518.1 GI:33815326  
 KEYWORDS  
 EST.  
 SOURCE  
 Oryza sativa

ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 1 (bases 1 to 27)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA

FEATURES  
 source  
 1. .27  
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 methyltransferase overexpression line."

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RESULT 583  
 CF333518  
 LOCUS  
 DEFINITION  
 JMT--02-H05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--02-H05, mRNA sequence.

ACCESSION  
 CF333518  
 VERSION  
 CF333518.1 GI:33815326  
 KEYWORDS  
 EST.  
 SOURCE  
 Oryza sativa

ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE  
 1 (bases 1 to 27)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA

FEATURES  
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 /tissue\_type="leaf"  
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 cDNA library (JMT)"  
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 prepared from Arabidopsis jasmonate Carboxyl  
 methyltransferase overexpression line."

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 Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 583  
 CF333518  
 LOCUS  
 DEFINITION  
 JMT--02-H05.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa cDNA clone JMT--02-H05, mRNA sequence.

ACCESSION  
 CF333518  
 VERSION  
 CF333518.1 GI:33815326  
 KEYWORDS  
 EST.  
 SOURCE  
 Oryza sativa

ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

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 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA

FEATURES  
 source  
 1. .27  
 /organism="Oryza sativa"  
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 /clone="JMT-02-H05"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="AtJMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis jasmonate Carboxyl  
 methyltransferase overexpression line."



**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

**JOURNAL** Unpublished (2000)

**COMMENT** Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0139 row: I column: 20  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 27.

**FEATURES**  
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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0139120"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 3.7e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 4463 CTTTTTTTTTTTTTTTTT 4482  
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**Db** 8 CTTTTTTTTTTTTTTTTT 27

**RESULT 587**  
**AZ654007**  
**LOCUS** 1M0527020R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
**DEFINITION** Clone UUGC1M0527020 R, genomic survey sequence.  
**ACCESSION** AZ654007  
**VERSION** AZ654007.1 GI:11791153  
**KEYWORDS** GSS.  
**SOURCE** Mus musculus (house mouse)  
**ORGANISM** Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 28)  
**REFERENCE** Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D. Weiss, R.  
**AUTHORS** Mouse whole genome scaffolding with paired end reads from 10kb

**JOURNAL** Unpublished (2000)

**COMMENT** Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0527 row: O column: 20  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 28.

**FEATURES**  
source  
1. .28  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
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/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 4e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**QY** 4466 TTTTTTTTTTTTTTTTCT 4485  
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**Db** 8 TTTTTTTTTTTTTTTTGT 27

**RESULT 588**  
**AL048694/C**  
**LOCUS** DKFZP566D043\_r1 566 (synonym: hfk2) Homo sapiens cDNA clone  
**DEFINITION** DKFZP566D043, mRNA sequence.  
**ACCESSION** AL048694  
**VERSION** AL048694.1 GI:4727765  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 29)  
**REFERENCE** Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.  
**AUTHORS** EST (Koehrer, et al.)  
**TITLE** Unpublished (1999)  
**JOURNAL** Contact: MIPS  
**COMMENT** MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES source Location/Qualifiers

1. .29

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DKFZp566D043"

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/notes="Vector: pAMP1; Site\_1: NotI; Site\_2: SalI"

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483

Db 29 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 10

RESULT 589

AL048741/c

LOCUS 29 bp mRNA linear EST 04-SEP-2003

DEFINITION DKFZp566G063\_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone

ACCESSION DKFZp566G063, mRNA sequence.

VERSION AL048741

KEYWORDS EST.

SOURCE AL048741.1 GI:4727812

ORGANISM Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 29)

AUTHORS Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

TITLE EST (Koehrer, et al.)

JOURNAL Unpublished (1999)

COMMENT Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

FEATURES source Location/Qualifiers

1. .29

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

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/notes="Vector: pAMP1; Site\_1: NotI; Site\_2: SalI"

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Best Local Similarity 100.0%; Pred. No. 4.3e+02;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483

Db 29 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 10

RESULT 590

CF292082

LOCUS 29 bp mRNA linear EST 14-AUG-2003

DEFINITION 14ROOT--02-M08.b1 Rice root plasmid cDNA library (14ROOT) Oryza sativa cDNA clone 14ROOT--02-M08, mRNA sequence.

ACCESSION CF292082

VERSION CF292082.1 GI:33661115

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE 1 (bases 1 to 29)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .29

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="14ROOT--02-M08"

/tissue\_type="root"

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/notes="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

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Best Local Similarity 82.1%; Pred. No. 4.3e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0

Qy 4455 GGCATGACACTTTTTTTTTTTTTTTTTTTTTTTT 4482

Db 2 GGCATGACACTGTTTTTTTTTTTTTTTTTTTTT 29

RESULT 591

CF295370

LOCUS 29 bp mRNA linear EST 14-AUG-2003

DEFINITION 30DGS--05-E14.g1 Rice leaf plasmid cDNA library 1 (30DGS) Oryza sativa cDNA clone 30DGS--05-E14, mRNA sequence.

ACCESSION CF295370

VERSION CF295370.1 GI:33664403

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 29)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 321 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

Location/Qualifiers

1. .29

/organism="Oryza sativa"

/mol\_type="mRNA"

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Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTT 4483
Db 29 TTTT...TTTTT 10

RESULT 589
AL048741/c           29 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFZp566J063_r1 566 (synonym: hfkd2) Homo sapiens cDNA clone
            DKFZp566J063, mRNA sequence.
ACCESSION AL048741
VERSION AL048741.1 GI:4727812
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 29)
AUTHORS Koehrer K., Beyer A., Mewes H.W., Gassenhuber J. and Wiemann S.
TITLE EST (Koehrer, et al.)
JOURNAL Unpublished (1999)
COMMENT Contact: MIPS
MIPS

FEATURES             Location/Qualifiers
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                       /db_xref="taxon:9606"
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                       /tissue_type="kidney"
                       /dev_stage="fetal"
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                       /notes="Vector: pAMP1; Site_1: NotI; Site_2: SalI"

Query Match          0.3%; Score 20; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT...TTTTT 4483
Db 29 TTTT...TTTTT 10

RESULT 590
CF292082            29 bp mRNA linear EST 14-AUG-2003
LOCUS 14ROOT--02-M08.b1 Rice root plasmid cDNA library (14ROOT) Oryza
DEFINITION sativa cDNA clone 14ROOT--02-M08, mRNA sequence.
ACCESSION CF292082
VERSION CF292082.1 GI:33661115
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

FEATURES             Location/Qualifiers
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Oryzatoideae; Oryzeae; Oryza.
1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Oryzatoideae; Oryzeae; Oryza.
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Oryzatoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Oryzatoideae; Oryzeae; Oryza.
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Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Oryzatoideae; Oryzeae; Oryza.
1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Oryzatoideae; Oryzeae; Oryza.
1 (bases 1 to 29)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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Oryzatoideae; Oryzeae; Oryza.
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Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

```

/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 29;  
Best Local Similarity 82.1%; Pred. No. 4.3e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4456 GCATGACACTTTTCTTTTCTTTTCTTTTCTTTT 4483  
||||| | | | | | | | | | | | | | | | | | | | |  
Db 1 GCATGACAGTGTCTTTTCTTTTCTTTTCTTTTCTTTT 28

RESULT 592  
CF295445  
LOCUS  
DEFINITION 29 bp mRNA linear EST 14-AUG-2003  
sativa cDNA clone 30DGS--05-G12, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
Location/Qualifiers

1. .29  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="30DGS--05-G12"  
/tissue\_type="leaf"  
/dev\_stage="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 20; DB 1; Length 29;  
Best Local Similarity 82.1%; Pred. No. 4.3e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4455 GGCATGACACTTTTCTTTTCTTTTCTTTTCTTTT 4482  
||||| | | | | | | | | | | | | | | | | | | | |  
Db 2 GGCATGACAGTGTCTTTTCTTTTCTTTTCTTTTCTTTT 29

RESULT 593  
CF306409/c  
LOCUS  
DEFINITION 29 bp mRNA linear EST 15-AUG-2003  
HDAL--03-M04.g1 OshDACL1-overexpressing transgenic rice lambda phage  
cDNA library I (HDAL) Oryza sativa cDNA clone HDAL--03-M04, mRNA  
sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

# REFERENCE

## AUTHORS

## JOURNAL

## COMMENT

1 (bases 1 to 29)  
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
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Contact: Nahm B.H.  
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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

# FEATURES

## source

Location/Qualifiers

1. .29  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="HDAL--03-M04"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OshDACL1-overexpressing transgenic rice lambda  
phage cDNA library I (HDAL)"  
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
was inserted into lambda Uni-ZAP XR vector at 5' end with  
EcoRI and 3' end with XhoI site. mRNA was derived from  
rice Histone Deacetylase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 29;  
Best Local Similarity 82.1%; Pred. No. 4.3e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4455 GGCATGACACTTTTCTTTTCTTTTCTTTTCTTTT 4482  
||||| | | | | | | | | | | | | | | | | | | | |  
Db 28 GGGGGGGGGTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 1

# RESULT 594

## LOCUS

## DEFINITION

29 bp DNA linear GSS 13-DEC-2000  
T. brucei sheared genomic DNA clone 239g06, reverse sequence,  
genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AL481179  
AL481179.1 GI:11846878  
GSS.  
Trypanosoma brucei  
Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

1 (bases 1 to 29)  
Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,  
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,  
Melville,S.E., Rajandream,M.A. and Barrell,B.G.  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

# REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available  
at [http://www.sanger.ac.uk/projects/T\\_brucei/](http://www.sanger.ac.uk/projects/T_brucei/).

## FEATURES

source  
1. .29  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/db\_xref="TREU927"  
/db\_xref="taxon:5691"  
/clone="239g06"

Query Match 0.3%; Score 20; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 4.3e+02; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0;

Qy 4463 CTTTTTTTTTTTTTTTTT 4482  
|||||  
Db 20 CTTTTTTTTTTTTTTTTT 1

RESULT 595  
AL048729/c  
LOCUS  
DEFINITION DKZP5661113.r1.566 (synonym: hfkd2) Homo sapiens cDNA clone  
DKZP5661113, mRNA sequence.

ACCESSION AL048729  
VERSION AL048729.1 GI:4727800

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S.

EST (Koehrer, et al.)

Unpublished (1999)

JOURNAL

COMMENT

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany.

## FEATURES

source  
1. .30  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="DKZP5661113"  
/tissue\_type="kidney"  
/dev\_stage="fetal"  
/lab\_host="Xl-2blue"  
/clone\_lib="566 (synonym: hfkd2)"  
/note="Vector: pAMP1; Site\_1: NotI; Site\_2: SalI"

Query Match 0.3%; Score 20; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4483  
|||||  
Db 30 TTTTTTTTTTTTTTTTTT 11

RESULT 596  
BX551781  
LOCUS  
DEFINITION BX551781 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tseilg01\_plc, mRNA sequence.

ACCESSION BX551781

VERSION BX551781.1 GI:33376108

KEYWORDS EST.

SOURCE

ORGANISM

Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Hippoboscidae; Glossinidae; Glossina.

1 (bases 1 to 30)

## AUTHORS

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

## CONTACT

## HALL N

## The Sanger Institute

## The Wellcome Trust Genome Campus

## Hinxton, Cambridge, CB10 1SA, UK

## Request for clones, please contact: Mike Lehane

## Prof. M.J. Lehane

## School of Biological Sciences,

## University of Wales,

## Bangor LL57 2UW

## All clones with suffix q1c are reverse primer reads starting at 5'

## end of the cDNA all plc reads are from

## the 3' end.

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All clones with suffix gic are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

#### FEATURES

source  
Location/Qualifiers  
1. .30  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tsel17re12\_pic"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected gut"  
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 20; DB 1; Length 30;  
Best Local Similarity 100.0%; Pred. No. 4.7e+02;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4465 TTTTCTTTTCTTTTCTTTG 4484

Db 11 TTTTCTTTTCTTTTCTTTG 30

#### RESULT 598

CF333289  
LOCUS  
DEFINITION JMT--02-C01.b1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-C01, mRNA sequence.

CF333289

VERSION CF333289.1 GI:33814856

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1. (bases 1 to 30)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

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Unpublished (2003)

Contact: Nahm B.H.

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

source  
Location/Qualifiers  
1. .30  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--02-C01"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
/note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.3%; Score 20; DB 1; Length 30;  
Best Local Similarity 82.1%; Pred. No. 4.7e+02;  
Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTG 4491

|||||

Db

#### RESULT 599

AZ604126/c

LOCUS

DEFINITION

clone UUGC1M0423013 R, genomic survey sequence.

ACCESSION

AZ604126

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .30

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0423013"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 30;

Best Local Similarity 82.1%; Pred. No. 4.7e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5699 TTTGCTCTCTTTTCTCTCTCTCTTT 5726

|||||

Db 29 TTTGCTCTCTCTTTTCTCTCTCTCTCT 2

2 TTTTCTTTTCTTTTCTTTCTTCTCGGAG 29

AZ604126

LOCUS

DEFINITION

clone UUGC1M0423013 R, genomic survey sequence.

ACCESSION

AZ604126

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1. .30

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0423013"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 20; DB 1; Length 30;

Best Local Similarity 82.1%; Pred. No. 4.7e+02;

Matches 23; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5699 TTTGCTCTCTTTTCTCTCTCTCTTT 5726

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Db 29 TTTGCTCTCTCTTTTCTCTCTCTCTCT 2



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RESULT 600
CF279593
LOCUS
DEFINITION
  CF279593
  14ETL--05-P06.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
  Oryza sativa cDNA clone 14ETL--05-P06, mRNA sequence.
ACCESSION
CF279593
VERSION
CF279593.1 GI:33656979
KEYWORDS
EST.
SOURCE
  Oryza sativa
  Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE
  1 (bases 1 to 23)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
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  Query Match 0.3%; Score 19.8; DB 1; Length 23;
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QY 4464 TTTTTCCTTTTTCCTTTTTCCTTTTC 4486
DB 1 TTTTTCCTTTTTCCTTTTTCCTTTTC 23

RESULT 601
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LOCUS
DEFINITION
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  HD--01-G01.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa cDNA clone HD--01-G01, mRNA sequence.
ACCESSION
CF313297
VERSION
CF313297.1 GI:33685058
KEYWORDS
EST.
SOURCE
  Oryza sativa
  Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE
  1 (bases 1 to 23)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
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  /lab_host="E.coli DH10B"
  /clone_lib="Rice etiolated leaf plasmid cDNA library
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  Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTTCCTTTTC 4486
DB 1 TTTTTCCTTTTTCCTTTTTCCTTTTC 23

RESULT 602
CF318266
LOCUS
DEFINITION
  CF318266
  HD--08-F07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa cDNA clone HD--08-F07, mRNA sequence.
ACCESSION
CF318266
VERSION
CF318266.1 GI:33690027
KEYWORDS
EST.
SOURCE
  Oryza sativa
  Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE
  1 (bases 1 to 23)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
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  /lab_host="E.coli DH10B"
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  cDNA library (HD)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
  treated with ABA(20um) for 1hr. Oligo-capped mRNA was
  reverse transcribed and then used for PCR. mRNA was
  derived from rice Histone Deacetylase overexpression
  line."

```

```

Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
  source
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  /clone="HD-01-G01"
  /tissue_type="callus"
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  /lab_host="E.coli DH10B"
  /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
  cDNA library (HD)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
  treated with ABA(20um) for 1hr. Oligo-capped mRNA was
  reverse transcribed and then used for PCR. mRNA was
  derived from rice Histone Deacetylase overexpression
  line."
  Query Match 0.3%; Score 19.8; DB 1; Length 23;
  Best Local Similarity 91.3%; Pred. No. 2.8e+02;
  Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTTCCTTTTC 4486
DB 1 TTTTTCCTTTTTCCTTTTTCCTTTTC 23

RESULT 602
CF318266
LOCUS
DEFINITION
  CF318266
  HD--08-F07.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
  library (HD) Oryza sativa cDNA clone HD--08-F07, mRNA sequence.
ACCESSION
CF318266
VERSION
CF318266.1 GI:33690027
KEYWORDS
EST.
SOURCE
  Oryza sativa
  Oryza sativa
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE
  1 (bases 1 to 23)
  Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
  Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
  Large-scale Sequencing Analysis of Rice ESTs
  Unpublished (2003)
  Contact: Nahm B.H.
  Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
  of Bioscience and Bioinformatics, Myongji University
  Yongin, Kyeonggi, Korea
  Tel: 82 31 330 6193
  Fax: 82 31 321 6355
  Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
  source
  1..23
  /organism="Oryza sativa"
  /mol_type="mRNA"
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  /tissue_type="callus"
  /dev_stage="proliferated callus on 2N6 media for 2 weeks"
  /lab_host="E.coli DH10B"
  /clone_lib="OshDAC1-overexpressing transgenic rice plasmid
  cDNA library (HD)"
  /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was
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  reverse transcribed and then used for PCR. mRNA was
  derived from rice Histone Deacetylase overexpression
  line."

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Query Match      0.3%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTT...TTTTTGCT 4487
DB 1 TTTT...TTTTTGCTT 23

RESULT 603
AZ607198/c
LOCUS
DEFINITION
1M0429G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0429G03 R, genomic survey sequence.
ACCESSION
AZ607198
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: G column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
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/sex="Male"
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 19.8; DB 1; Length 23;
Best Local Similarity 91.3%; Pred. No. 2.8e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTT...TTTTTGCT 4487
DB 1 TTTT...TTTTTGCTT 23

RESULT 603
AZ607198/c
LOCUS
DEFINITION
1M0429G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0429G03 R, genomic survey sequence.
ACCESSION
AZ607198
VERSION
KEYWORDS
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0429 row: G column: 03
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0429G03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 19.8; DB 1; Length 24;
Best Local Similarity 91.3%; Pred. No. 3e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4465 TTTT...TTTTTGCT 4487
DB 24 TTTT...TTTTTGCTT 2

RESULT 604
CF326989
LOCUS
DEFINITION
NACL--01-E15.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--01-E15, mRNA sequence.
ACCESSION
CF326989
VERSION
KEYWORDS
SOURCE
Oryza sativa
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartioideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 25)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Mahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.
Location/Qualifiers
1..25
/organism="Oryza sativa"
/mol_type="mRNA"
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with oligoribonucleotides and then used as templates for
RT-PCR."
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Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhauser, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0004 row: A column: 01  
 Seq primer: CGTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 25.

#### FEATURES

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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19.8; DB 1; Length 25;  
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RESULT 606  
 BX555317 28 bp mRNA linear EST 10-OCT-2003  
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 DEFINITION BX555317  
 ACCESSION BX555317  
 VERSION BX555317.1 GI:33379318  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 28)  
 AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

#### TITLE

JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes  
 Genome Biol. 4 (10), R63 (2003)  
 22881942  
 14519198  
 Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

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Query Match 0.3%; Score 19.8; DB 1; Length 28;  
 Best Local Similarity 91.3%; Pred. No. 4.3e+02;  
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Qy 4460 GGACTTTTCTTTTCTTTTCTTTTCTTTT 4482  
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RESULT 607  
 CF293772 29 bp mRNA linear EST 14-AUG-2003  
 LOCUS CF293772 30DGS--03-B05.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza sativa cDNA clone 30DGS--03-B05, mRNA sequence.  
 DEFINITION CF293772  
 ACCESSION CF293772  
 VERSION CF293772.1 GI:33662805  
 KEYWORDS EST.

SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 29)  
 AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 TITLE Large-scale Sequencing Analysis of Rice ESTs  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

#### FEATURES

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Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 4 TAGATAGTTTTTTTTTTTTTTTTTTTGG 29

RESULT 613
BX555418 29 bp mRNA linear EST 10-OCT-2003
DEFINITION BX555418 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse2d06_pic, mRNA sequence.
ACCESSION BX555418
VERSION    BX555418.1 GI:33379412
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 29)
AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PUBMED    14519198
COMMENT   Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxtion, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all pic reads are from
            the 3' end.

FEATURES             source
    source
    1..29
    /organism="Glossina morsitans morsitans"
    /mol_type="mRNA"
    /sub_species="morsitans"
    /db_xref="taxon:37546"
    /clone="Tse2d06_pic"
    /tissue_type="adult infected gut"
    /clone_lib="Glossina morsitans morsitans adult infected
    gut"
    /notes="country: Zimbabwe; EST from adult gut infected with
    T.brucei"

    Query Match      0.3%; Score 19.6; DB 1; Length 29;
    Best Local Similarity 84.6%; Pred. No. 5e+02;
    Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

    Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTTGG 4484
        ||| ||||| ||||| ||||| |||||
    Db 4 TAGATAGTTTTTTTTTTTTTTTTTTTGG 29

RESULT 613
BX556473 29 bp mRNA linear EST 10-OCT-2003
DEFINITION BX556473 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse2d01_pic, mRNA sequence.
ACCESSION BX556473
VERSION    BX556473.1 GI:33427734
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 29)
AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PUBMED    14519198
COMMENT   Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxtion, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all pic reads are from
            the 3' end.

    Query Match      0.3%; Score 19.6; DB 1; Length 29;
    Best Local Similarity 84.6%; Pred. No. 5e+02;
    Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

    Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTTGG 4484
        ||| ||||| ||||| ||||| |||||
    Db 4 TAGATAGTTTTTTTTTTTTTTTTTTTGG 29

RESULT 614
BX556473 29 bp mRNA linear EST 10-OCT-2003
DEFINITION BX556473 Glossina morsitans morsitans adult infected gut Glossina
            morsitans morsitans cDNA clone Tse2d01_pic, mRNA sequence.
ACCESSION BX556473
VERSION    BX556473.1 GI:33427734
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 29)
AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PUBMED    14519198
COMMENT   Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxtion, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all pic reads are from
            the 3' end.

```

```

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 29)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
        Pathogen Sequencing Unit
        The Sanger Institute The Wellcome Trust Genome Campus
        Hinxtion, Cambridge, CB10 1SA, UK
        Request for clones, please contact: Mike Lehane
        Prof. M.J.Lehane
        School of Biological Sciences,
        University of Wales,
        Bangor LL57 2UW
        All clones with suffix q1c are reverse primer reads starting at 5'
        end of the cDNA all pic reads are from
        the 3' end.

FEATURES             source
    source
    1..29
    /organism="Glossina morsitans morsitans"
    /mol_type="mRNA"
    /sub_species="morsitans"
    /db_xref="taxon:37546"
    /clone="Tse2d01_pic"
    /tissue_type="adult infected gut"
    /clone_lib="Glossina morsitans morsitans adult infected
    gut"
    /notes="country: Zimbabwe; EST from adult gut infected with
    T.brucei"

    Query Match      0.3%; Score 19.6; DB 1; Length 29;
    Best Local Similarity 84.8%; Pred. No. 5e+02;
    Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

    Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTTGG 4484
        ||| ||||| ||||| ||||| |||||
    Db 4 TAGATAGTTTTTTTTTTTTTTTTTTTGG 29

RESULT 615
BX567852 29 bp mRNA linear EST 14-OCT-2003
LOCUS     BX567852 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse8d11_pic, mRNA sequence.
ACCESSION BX567852
VERSION    BX567852.1 GI:33434762
KEYWORDS   EST.
SOURCE     Glossina morsitans morsitans
ORGANISM   Glossina morsitans morsitans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 29)
AUTHORS   Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
            Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE     Adult midgut expressed sequence tags from the tsetse fly Glossina
            morsitans morsitans and expression analysis of putative immune
            response genes
JOURNAL   Genome Biol. 4 (10), R63 (2003)
MEDLINE   22881942
PUBMED    14519198
COMMENT   Contact: Hall N
            Pathogen Sequencing Unit
            The Sanger Institute The Wellcome Trust Genome Campus
            Hinxtion, Cambridge, CB10 1SA, UK
            Request for clones, please contact: Mike Lehane
            Prof. M.J.Lehane
            School of Biological Sciences,
            University of Wales,
            Bangor LL57 2UW
            All clones with suffix q1c are reverse primer reads starting at 5'
            end of the cDNA all pic reads are from
            the 3' end.

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Query Match		0.3%	Score 19.6;	DB 1;	Length 30;
Best Local Similarity		84.6%;	Pred. No. 5.4e+02;		
Matches		22;	Conservative	0;	Mismatches 4; Indels 0; Gaps 0;
Qy	4459	TTGACATTTT	TTTTTTTTTTTTTTTTTTT	TTTGGT	4484
Db	4	TAGATAGTTT	TTTTTTTTTTTTTTTTTTT	TTTGGT	29
<p>RESULT 617</p> <p>CF276747</p> <p>LOCUS</p> <p>DEFINITION</p> <p>ACCESSION</p> <p>VERSION</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p> <p>REFERENCE</p> <p>AUTHORS</p> <p>TITLE</p> <p>JOURNAL</p> <p>COMMENT</p>					
<p>CF276747 21 bp mRNA linear EST 14-AUG-2003</p> <p>14ETL--02-A06.b1 Rice etiolated leaf plasmid cDNA library (14ETL)</p> <p>Oryza sativa cDNA clone 14ETL--02-A06, mRNA sequence.</p> <p>CF276747 CF276747.1 GI:33654133</p> <p>EST.</p> <p>Oryza sativa</p> <p>Oryza sativa</p> <p>Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.</p> <p>1 (bases 1 to 21)</p> <p>Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.</p> <p>Large-scale Sequencing Analysis of Rice ESTs</p> <p>Unpublished (2003)</p> <p>Contact: Nahm B.H.</p> <p>Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University</p> <p>Yongin, Kyeonggi, Korea</p> <p>Tel: 82 31 330 6193</p> <p>Fax: 82 31 321 6355</p> <p>Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.</p>					
<p>FEATURES</p> <p>source</p> <p>1..21</p> <p>/organism="Oryza sativa"</p> <p>/mol_type="mRNA"</p> <p>/cultivar="Nackdong"</p> <p>/db_xref="taxon:4530"</p> <p>/clone="14ETL--02-A06"</p> <p>/tissue_type="leaf"</p> <p>/dev_stage="14 days after germination"</p> <p>/lab_host="E.coli DH10B"</p> <p>/clone_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"</p> <p>/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."</p>					
<p>Query Match 0.3%; Score 19.4; DB 1; Length 21;</p> <p>Best Local Similarity 95.2%; Pred. No. 2.6e+02;</p> <p>Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;</p>					
Qy	4465	TTTTTTTTTTTTTTTTTTT	TTTTTTT	TTTGGT	4485
Db	1	TTTTTTTTTTTTTTTTTTT	TTTTTTT	TTTGGT	21
<p>RESULT 618</p> <p>AZ493766/c</p> <p>LOCUS</p> <p>DEFINITION</p> <p>ACCESSION</p> <p>VERSION</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p>					
<p>AZ493766 21 bp DNA linear GSS 05-OCT-2000</p> <p>1M0328C11r Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0328C11 R, genomic survey sequence.</p> <p>AZ493766</p> <p>AZ493766.1 GI:10667750</p> <p>GSS.</p> <p>Mus musculus (house mouse)</p> <p>Mus musculus</p> <p>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p>					







```

JOURNAL      plasmid inserts
COMMENT      Unpublished (2000)
             Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0560 row: H column: 02
             Seq primer: CACACAGAAACACGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 24.

FEATURES             source
    Location/Qualifiers
        1..24
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0560H02"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adapted DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adapted mouse DNA was annealed to
            adapted vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

Query Match      0.3%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4482
Db      21 AATTTTCTTTTCTTTTCTTTTCTTTT 1

RESULT 624
LOCUS      A2764513 24 bp DNA linear GSS 16-FEB-2001
DEFINITION      IM0560D11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                clone UUGC1M0560D11 R, genomic survey sequence.
VERSION      A2764513
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      1 (bases 1 to 24)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts

JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
             University of Utah Genome Center
             University of Utah
             Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
             84112, USA
             Tel: 801 585 5606
             Fax: 801 585 7177
             Email: ddunn@genetics.utah.edu
             Insert Length: 10000 Std Error: 0.00
             Plate: 0560 row: D column: 11
             Seq primer: CACACAGAAACACGCTATGACC
             Class: plasmid ends
             High quality sequence stop: 24.

FEATURES             source
    Location/Qualifiers
        1..24
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC1M0560D11"
            /sex="Male"
            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC1M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (male) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adapted DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adapted mouse DNA was annealed to
            adapted vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."

Query Match      0.3%; Score 19.4; DB 1; Length 24;
Best Local Similarity 95.2%; Pred. No. 3.6e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4482
Db      21 AATTTTCTTTTCTTTTCTTTTCTTTT 1

RESULT 625
LOCUS      AV737092 25 bp mRNA linear EST 17-OCT-2000
DEFINITION      AV737092 CB Homo sapiens cDNA clone CBFIB11 5', mRNA sequence.
VERSION      AV737092
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE      1 (bases 1 to 25)
AUTHORS      Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
            Chen,S., Mao,M. and Chen,Z.
TITLE      Homo sapiens CB library cDNA clones
JOURNAL      Unpublished (2000)
COMMENT      Contact: Zhu Chen
            Shanghai Institute of Hematology, Rui-Jin Hospital
            197 Rui-Jin II Road, Shanghai 200025, P. R. China
            Tel: 86-21-64740490

```

```

Fax: 86-21-64743206
Email: mbshims@stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
1. 25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBFBIB1"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
/notes="Vector: pBluescript; Site 1: EcoRI; The insert is
cloned randomly with the EcoRI digestion"
Query Match 0.3%; Score 19.4; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTTCTTGT 4485
Db 25 TTTTCTTTTCTTTTCTTTTCTTGT 4

RESULT 626
TA388E06P/c 25 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 388e06, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL498782
VERSION AL498782.1 GI:11874504
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 25)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajadream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. 25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="388e06"

FEATURES
source
Query Match 0.3%; Score 19.4; DB 1; Length 25;
Best Local Similarity 95.2%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Thu Oct 14 15:43:37 2004
Fax: 86-21-64743206
Email: mbshims@stn.sh.cn
This clone is available at Shanghai Hematology Institute in
Shanghai.
Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi- Tech Park, Pudong.
Location/Qualifiers
1. 25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CBFBIB1"
/tissue_type="cord blood"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
/clone_lib="CB"
/notes="Vector: pBluescript; Site 1: EcoRI; The insert is
cloned randomly with the EcoRI digestion"
Query Match 0.3%; Score 19.4; DB 1; Length 25;
Best Local Similarity 90.9%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTTCTTGT 4485
Db 25 TTTTCTTTTCTTTTCTTTTCTTGT 4

RESULT 626
TA388E06P/c 25 bp DNA linear GSS 13-DEC-2000
LOCUS T. brucei sheared genomic DNA clone 388e06, forward sequence,
DEFINITION genomic survey sequence.
ACCESSION AL498782
VERSION AL498782.1 GI:11874504
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
1 (bases 1 to 25)
Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajadream, M.A. and Barrell, B.G.
Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nh@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v + i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
1. 25
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="388e06"

FEATURES
source
Query Match 0.3%; Score 19.4; DB 1; Length 25;
Best Local Similarity 95.2%; Pred. No. 3.9e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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```

Qy 4463 CTTTCTTTTCTTTTCTTTTCTTGT 4483
Db 21 CTTCTTTTCTTTTCTTTTCTTGT 1

RESULT 627
CF309933/c 26 bp mRNA linear EST 15-AUG-2003
LOCUS ABF--04-F09.g1 ABF3-overexpressing transgenic rice plasmid cDNA
DEFINITION library (ABF) Oryza sativa cDNA clone ABF--04-F09, mRNA sequence.
ACCESSION CF309933
VERSION CF309933.1 GI:33681694
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 320 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. 26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--04-F09"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
Query Match 0.3%; Score 19.4; DB 1; Length 26;
Best Local Similarity 95.2%; Pred. No. 4.3e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTTCTTGT 4482
Db 21 AGTTTCTTTTCTTTTCTTTTCTTGT 1

RESULT 628
AZ764502/c 26 bp DNA linear GSS 16-FEB-2001
LOCUS 1M0560L03R Mouse 10kb plasmid UGCM library Mus musculus genomic
DEFINITION clone UGCM1M0560L03 R, genomic survey sequence.
ACCESSION AZ764502
VERSION AZ764502.1 GI:12879531
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, S., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

```

**TITLE** Niederhauser, A. and Wright, D., Weiss, R.  
**JOURNAL** Mouse whole genome scaffolding with paired end reads from 10kb  
**COMMENT** plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0560 row: L column: 03  
 Seq primer: CACACAGGAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 26.

**FEATURES** Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0560L03"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19.4; DB 1; Length 26;  
 Best Local Similarity 95.2%; Pred. No. 4.3e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 4462 ACTTTTTTTTTTTTTTTTTT 4482  
**Db** 21 AATTTTTTTTTTTTTTTTTT 1

**RESULT** 629  
**LOCUS** BX554747 28 bp mRNA linear EST 10-OCT-2003  
**DEFINITION** morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse17c01\_plc, mRNA sequence.  
**ACCESSION** BX554747  
**VERSION** BX554747.1 GI:33378810  
**KEYWORDS** EST.  
**SOURCE** Glossina morsitans morsitans  
**ORGANISM** Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
**REFERENCE** 1 (bases 1 to 28)  
**AUTHORS** Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
**TITLE** Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune response genes  
 Genome Biol. 4 (10), R63 (2003)  
 22881942  
 14519198  
**COMMENT** Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

**FEATURES** Location/Qualifiers  
 source 1..28  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
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 /db\_xref="taxon:37546"  
 /clone="Tse17c01\_plc"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 28;  
 Best Local Similarity 95.2%; Pred. No. 5e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy** 4464 TTTTTTTTTTTTTTTTTT 4484  
**Db** 8 TGTTCATTTTTTTTTTTT 28

**RESULT** 630  
**LOCUS** BX555569 28 bp mRNA linear EST 10-OCT-2003  
**DEFINITION** Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse21e01\_plc, mRNA sequence.  
**ACCESSION** BX555569  
**VERSION** BX555569.1 GI:33379552  
**KEYWORDS** EST.  
**SOURCE** Glossina morsitans morsitans  
**ORGANISM** Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
**REFERENCE** 1 (bases 1 to 28)  
**AUTHORS** Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
**TITLE** Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

**JOURNAL** Genome Biol. 4 (10), R63 (2003)  
**MEDLINE** 22881942  
**PUBMED** 14519198  
**COMMENT** Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 29)  
**REFERENCE** NIH-MGC <http://mgc.nci.nih.gov/>.  
**AUTHORS** National Institutes of Health, Mammalian Gene Collection (MGC)  
**TITLE** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-x@mail.nih.gov](mailto:cgabs-x@mail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Edge Biosystems  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: NIH Intramural Sequencing Center (NISC)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio-llnl.gov/bbrp/image/image.html](http://bio-llnl.gov/bbrp/image/image.html)  
 Plate: LLCW0028 row: L column: 18  
 Seq primer: -21M13 forward primer (ABI).  
**FEATURES** Location/Qualifiers  
 1..29  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2846753"  
 /tissue\_type="T cell leukemia"  
 /cell\_line="MGC2"  
 /clone\_lib="NIH\_MGC\_2"  
 /notes="Organ: Blood; Vector: pOTB7a; Library prepared by  
 Edge Biosystems."  
 Query Match 0.3%; Score 19.4; DB 1; Length 29;  
 Best Local Similarity 95.2%; Pred: No. 5.4e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
**QY** 4466 TTTTITTTTTTTTTTTTGGTC 4486  
 |||||  
**Db** 29 TTTTITTTTTTTTTTTTGGTC 9  
**RESULT** 633  
**EX549814**  
**LOCUS** EX549814 Glossina morsitans morsitans adult infected gut Glossina  
**DEFINITION** morsitans morsitans cDNA clone Tse10c03\_plc, mRNA sequence.  
**ACCESSION** BX549814  
**VERSION** BX549814.1 GI:33369063  
**KEYWORDS** EST.  
**ORGANISM** Glossina morsitans morsitans  
 Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 29)  
**REFERENCE** Lehane, M.J., Aksoy, S., Gibson, W., Kerkhoun, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
**AUTHORS** Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes  
**TITLE** Genome Biol. 4 (10), R63 (2003)  
**JOURNAL** 22881942  
**MEDLINE** 14519198  
**PUBMED** 14519198  
**COMMENT** Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix g1c are reverse primer reads starting at 5',



Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

#### REFERENCE AUTHORS

1 (bases 1 to 29)  
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

#### TITLE

Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

#### JOURNAL MEDLINE PUBMED

Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198

#### COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

#### FEATURES

source

Location/Qualifiers

1..29  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
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/db\_xref="taxon:37546"  
/clone="Tset128h03\_plc"  
/tissue\_type="adult infected gut"  
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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 29;  
Best Local Similarity 95.2%; Pred. No. 5.4e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4482

Db 9 AGTTTTTCTTTTCTTTTCTTTTCTTTT 29

#### RESULT 637 BX554178

LOCUS BX554178 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tset13h04\_plc, mRNA sequence.  
DEFINITION

#### ACCESSION

BX554178

#### VERSION

BX554178.1 GI:33378274

#### KEYWORDS

#### SOURCE

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

#### REFERENCE

1 (bases 1 to 29)  
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

#### JOURNAL MEDLINE PUBMED

Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198

#### COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

#### FEATURES

source

Location/Qualifiers

1..29  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
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/clone="Tset13h04\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected gut"  
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 29;  
Best Local Similarity 95.2%; Pred. No. 5.4e+02;  
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4482

Db 9 AGTTTTTCTTTTCTTTTCTTTTCTTTT 29

#### RESULT 638 BX554562

LOCUS BX554562 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tset16b01\_plc, mRNA sequence.  
DEFINITION

#### ACCESSION

BX554562

#### VERSION

BX554562.1 GI:33378635

#### KEYWORDS

#### SOURCE

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
1 (bases 1 to 29)  
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

#### JOURNAL MEDLINE PUBMED

Genome Biol. 4 (10), R63 (2003)  
22881942  
14519198

#### COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

#### FEATURES

source

Location/Qualifiers

1..29  
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/mol\_type="mRNA"  
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/db\_xref="taxon:37546"  
/clone="Tset16b01\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected gut"









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FEATURES
source
Location/Qualifiers
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/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/cloned_lib="Tse27f12_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match
Best Local Similarity 0.3%; Score 19.4; DB 1; Length 29;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTTTT 4482
DB 9 AGTTTTTTTTTTTTTTTTTTT 29

RESULT 647
BX556517
LOCUS
DEFINITION
Glossina morsitans morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse27f12_plc, mRNA sequence.
ACCESSION
BX556517
KEYWORDS
EST.
SOURCE
Glossina morsitans morsitans
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 29)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)
22881942
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COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES
source
Location/Qualifiers
1..29
/organism="Glossina morsitans morsitans"
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/sub_species="morsitans"
/db_xref="taxon:37546"
/cloned_lib="Tse27f12_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected gut"
/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match
Best Local Similarity 0.3%; Score 19.4; DB 1; Length 29;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTTTT 4482
DB 9 AGTTTTTTTTTTTTTTTTTTT 29

RESULT 648
BX556670
LOCUS
DEFINITION
Glossina morsitans morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse28g01_plc, mRNA sequence.
ACCESSION
BX556670
KEYWORDS
EST.
SOURCE
Glossina morsitans morsitans
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 29)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N. Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
Genome Biol. 4 (10), R63 (2003)
22881942
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COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qlc are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES
source
Location/Qualifiers
1..29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/cloned_lib="Tse28g01_plc"
/tissue_type="adult infected gut"
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/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match
Best Local Similarity 0.3%; Score 19.4; DB 1; Length 29;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTTTT 4482
DB 9 AGTTTTTTTTTTTTTTTTTTT 29

RESULT 649
BX557474
LOCUS
DEFINITION
Glossina morsitans morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse32f03_plc, mRNA sequence.
ACCESSION
BX557474
KEYWORDS
EST.
SOURCE
Glossina morsitans morsitans
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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FEATURES
  source
    Location/Qualifiers
      1..29
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        /sub_species="morsitans"
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        /clone="Tse27e07_plc"
        /tissue_type="adult infected gut"
        /clone_lib="Glossina morsitans morsitans adult infected gut"
        /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match
Best Local Similarity 0.3%; Score 19.4; DB 1; Length 29;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482
Db 9 AGTTTTTTTTTTTTTTTTT 29

RESULT 647
BX556517
LOCUS
DEFINITION
  Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse27f12_plc, mRNA sequence.
ACCESSION
  BX556517
KEYWORDS
  EST.
SOURCE
  Glossina morsitans morsitans
  ORGANISM
    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.
  1 (bases 1 to 29)
  Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
  Genome Biol. 4 (10), R63 (2003)
  22881942
  14519198
  PUBMED
  COMMENT
    Contact: Hall N
    Pathogen Sequencing Unit
    The Sanger Institute The Wellcome Trust Genome Campus
    Hinxton, Cambridge, CB10 1SA, UK
    Request for clones, please contact: Mike Lehane
    Prof. M.J.Lehane
    School of Biological Sciences,
    University of Wales,
    Bangor LL57 2UW
  REFERENCE
    1 (bases 1 to 29)
  AUTHORS
    Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  TITLE
    Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
  JOURNAL
    Genome Biol. 4 (10), R63 (2003)
  MEDLINE
    22881942
  PUBMED
    14519198
  COMMENT
    Contact: Hall N
    Pathogen Sequencing Unit
    The Sanger Institute The Wellcome Trust Genome Campus
    Hinxton, Cambridge, CB10 1SA, UK
    Request for clones, please contact: Mike Lehane
    Prof. M.J.Lehane
    School of Biological Sciences,
    University of Wales,
    Bangor LL57 2UW
  All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Glossina morsitans morsitans"
        /mol_type="mRNA"
        /sub_species="morsitans"
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        /clone="Tse27f12_plc"
        /tissue_type="adult infected gut"
        /clone_lib="Glossina morsitans morsitans adult infected gut"
        /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match
Best Local Similarity 0.3%; Score 19.4; DB 1; Length 29;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482
Db 9 AGTTTTTTTTTTTTTTTTT 29

RESULT 648
BX556670
LOCUS
DEFINITION
  Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse28g01_plc, mRNA sequence.
ACCESSION
  BX556670
KEYWORDS
  EST.
SOURCE
  Glossina morsitans morsitans
  ORGANISM
    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscoidae; Glossinidae; Glossina.
  1 (bases 1 to 29)
  Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M., Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
  Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes
  Genome Biol. 4 (10), R63 (2003)
  22881942
  14519198
  PUBMED
  COMMENT
    Contact: Hall N
    Pathogen Sequencing Unit
    The Sanger Institute The Wellcome Trust Genome Campus
    Hinxton, Cambridge, CB10 1SA, UK
    Request for clones, please contact: Mike Lehane
    Prof. M.J.Lehane
    School of Biological Sciences,
    University of Wales,
    Bangor LL57 2UW
  All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES
  source
    Location/Qualifiers
      1..29
        /organism="Glossina morsitans morsitans"
        /mol_type="mRNA"
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        /db_xref="taxon:37546"
        /clone="Tse28g01_plc"
        /tissue_type="adult infected gut"
        /clone_lib="Glossina morsitans morsitans adult infected gut"
        /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match
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Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482
Db 9 AGTTTTTTTTTTTTTTTTT 29

RESULT 649
BX557474
LOCUS
DEFINITION
  Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse32f03_plc, mRNA sequence.
ACCESSION
  BX557474
KEYWORDS
  EST.
SOURCE
  Glossina morsitans morsitans
  ORGANISM
    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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Query Match      0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 95.2%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4482
DB 9 AGTTTTTTTTTTTTTTTTTTTTTTT 29

RESULT 652
BX557758
LOCUS
DEFINITION
BX557758 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse34e06_plc, mRNA sequence.
ACCESSION
BX557758
VERSION
BX557758.1 GI:33428933
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 29)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
PUBMED
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse34e06_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T. brucei"

Query Match      0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 95.2%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4482
DB 9 AGTTTTTTTTTTTTTTTTTTTTTTT 29

RESULT 654
BX558583
LOCUS
DEFINITION
BX558583 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse39e03_plc, mRNA sequence.
ACCESSION
BX558583
VERSION
BX558583.1 GI:33365424
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 29)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
PUBMED
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit

```

```

KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 29)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
PUBMED
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J. Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all plc reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..29
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse35f10_plc"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T. brucei"

Query Match      0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 95.2%; Pred. No. 5.4e+02;
Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTCTTTTCTTTTCTTTTCTTTT 4482
DB 9 AGTTTTTTTTTTTTTTTTTTTTTTT 29

RESULT 654
BX558583
LOCUS
DEFINITION
BX558583 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse39e03_plc, mRNA sequence.
ACCESSION
BX558583
VERSION
BX558583.1 GI:33365424
KEYWORDS
SOURCE
ORGANISM
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE
1 (bases 1 to 29)
Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
PUBMED
14519198
COMMENT
Contact: Hall N
Pathogen Sequencing Unit

```

The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J.Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all plc reads are from  
 the 3' end.

## FEATURES

source

1. .29  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse39e03\_plc"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected  
 gut"  
 /notes="country: Zimbabwe; EST from adult gut infected with  
 T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 29;  
 Best Local Similarity 95.2%; Pred. No. 5.4e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482

Db 9 AGTTTTTTTTTTTTTTTTT 29

RESULT 655

BX562299

LOCUS

DEFINITION BX562299 Glossina morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone Tse3h07\_plc, mRNA sequence.

ACCESSION

BX562299

VERSION

BX562299.1 GI:33372596

KEYWORDS

EST.

SOURCE

ORGANISM

Glossina morsitans morsitans  
 Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 29)  
 Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J.Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all plc reads are from  
 the 3' end.

FEATURES

source

1. .29  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse5h07\_plc"

/tissue type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected  
 gut"  
 /notes="country: Zimbabwe; EST from adult gut infected with  
 T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 29;  
 Best Local Similarity 95.2%; Pred. No. 5.4e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482

Db 9 AGTTTTTTTTTTTTTTTTT 29

RESULT 656

BX563480

LOCUS

DEFINITION BX563480 Glossina morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone Tse67b04\_plc, mRNA sequence.

ACCESSION

BX563480

VERSION

BX563480.1 GI:33430708

KEYWORDS

EST.

SOURCE

ORGANISM

Glossina morsitans morsitans  
 Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 29)  
 Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,  
 Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.  
 Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J.Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all plc reads are from  
 the 3' end.

FEATURES

source

1. .29  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse67b04\_plc"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected  
 gut"  
 /notes="country: Zimbabwe; EST from adult gut infected with  
 T.brucei"

Query Match 0.3%; Score 19.4; DB 1; Length 29;  
 Best Local Similarity 95.2%; Pred. No. 5.4e+02;  
 Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4462 ACTTTTTTTTTTTTTTTTTT 4482

Db 9 AGTTTTTTTTTTTTTTTTT 29

RESULT 657

CF336137

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LOCUS       CF336137                29 bp    mRNA    linear    EST 18-AUG-2003
DEFINITION  JMT--06-B10.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--06-B10, mRNA sequence.
ACCESSION   CF336137
VERSION     CF336137.1    GI:33820654
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Oryza sativa
REFERENCE   1 (bases 1 to 29)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES             source
    1..29
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"
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    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli DH10B"
    /clone_lib="AtJMT-overexpressing transgenic rice plasmid
            cDNA library (JMT)"
    /note="Vector: pCR4-TOPO, Site.1: EcoRI; Oligo-capped mRNA
            was reverse transcribed and then used for PCR. mRNA was
            prepared from Arabidopsis Jasmonate Carboxyl
            methyltransferase overexpression line."

Query Match      0.3%; Score 19.4; DB 1; Length 29;
Best Local Similarity 79.3%; Pred. No. 5.4e+02;
Matches 23; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy  4457 CATGACATTTTTTTTTTTTTTTTTTTTGT 4485
Db  1 CATGACAGTGTGTGTGTGTGTGTGTGTGT 29

RESULT 658
LOCUS     AW247159                24 bp    mRNA    linear    EST 07-JAN-2000
DEFINITION  2819627.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819627 3',
            mRNA sequence.
ACCESSION   AW247159
VERSION     AW247159.1    GI:6590152
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
            Homo sapiens
ORGANISM    Homo sapiens
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 24)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Other ESTs: 2819627.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:

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www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center. Vector
PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 24
contiguous PHRED high quality bases following vector sequence. Very
Low Quality Sequence: Trace file contained 24 contiguous distinct
peaks following vector sequence. Polyadenylation: Based upon the
presence of a XhoI site followed by a run of 14 or more T residues
at the beginning of the sequence, this cDNA insert was
polyadenylated.
Plate: LCM2 row: B column: 12
High quality sequence stop: 24.
Location/Qualifiers
    1..24
    /organism="Homo sapiens"
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    /cell_line="MGC3"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH_MGC_7"
    /note="Organ: lung; Vector: pOTB7; Site.1: XhoI; Site.2:
            EcoRI; cDNA made by oligo-dT priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5'
            adaptor: GGCACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies)."

Query Match      0.3%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy  4464 TTTTGTGTGTGTGTGTGTGTGTGTGTGT 4487
Db  1 TTTTGTGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 659
LOCUS     CF281313                24 bp    mRNA    linear    EST 14-AUG-2003
DEFINITION  14ETL--08-F05.g1 Rice etiolated leaf plasmid cDNA library (14ETL)
            Oryza sativa cDNA clone 14ETL--08-F05, mRNA sequence.
ACCESSION   CF281313
VERSION     CF281313.1    GI:33658700
KEYWORDS    EST.
SOURCE      Oryza sativa
            Oryza sativa
ORGANISM    Oryza sativa
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 24)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnaheggbio.com, bhnaheggbio.myongji.ac.kr.

FEATURES             source
    1..24
    /organism="Oryza sativa"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:4530"

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/clone="14ETL--08-F05"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="vector: PCR4--TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTTTCCTTTTTCCTTTTTCCT 4487
      |||||
Db 1 TTTTTCCTTTTTCCTTTTTCCT 24

RESULT 660
AZ458112
LOCUS      24 bp      DNA      linear      GSS 04-OCT-2000
DEFINITION      IM0261E24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0261E24 R, genomic survey sequence.
ACCESSION      AZ458112
VERSION      AZ458112.1 GI:10616237
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0261 row: E column: 24
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0261E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

FEATURES
source
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0261E24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match      0.3%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred. No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4464 TTTTTCCTTTTTCCTTTTTCCT 4487
      |||||
Db 1 TTTTTCCTTTTTCCTTTTTCCT 24

RESULT 661
AZ486788
LOCUS      24 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION      IM0315122F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0315122 F, genomic survey sequence.
ACCESSION      AZ486788
VERSION      AZ486788.1 GI:10653906
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: I column: 22
Seq primer: CGTTGTAAAACGACGGCAGT
Class: plasmid ends
High quality sequence stop: 24.
Location/Qualifiers
1. .24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0315122"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative

```



inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* X10-Gold (Stratagene) cells and selected for ampicillin resistance."

```
Query Match      0.3%; Score 19.2; DB 1; Length 24;
Best Local Similarity 87.5%; Pred.No. 3.9e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

RESULT	663
AZ427752/c	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

```

FEATURES
source
1. .25
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0209N21"
/sex="Male"
/lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/vector="PBD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

```

with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.3%; Score 19.2; DB 1; Length 25;  
Best Local Similarity 87.5%; Pred. No. 4.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4465 TTTTTCCTTTTTCCTTCCTT 4488  
|||||  
Db 25 TTTTTCCTTTTTCCTTCCTT 2

RESULT 664  
BZ767540  
LOCUS  
DEFINITION SALK\_139012.18.15.n Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_139012.18.15.n, genomic survey sequence.

ACCESSION BZ767540  
VERSION BZ767540.1 GI:28940093  
KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 25)  
Alonso J.M., Leisse T.J., Barajas P., Chen H., Cheuk R.,  
Gadrinab C., Jenke A., Karnes M., Kim C.J., Parker H., Prednis L.,  
Shinn P., Zimmerman J. and Ecker J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

JOURNAL Arabidopsis Genome

COMMENT Unpublished (2001)

Contact: Joseph R. Ecker  
Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. .25  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/strain="Columbia 0"  
/db\_xref="taxon:3702"

/clone="SALK\_139012.18.15.n"  
/note="Arabidopsis thaliana TDNA insertion lines"  
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

Query Match 0.3%; Score 19.2; DB 1; Length 25;  
Best Local Similarity 87.5%; Pred. No. 4.2e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4465 TTTTTCCTTTTTCCTTCCTT 4488  
|||||  
Db 1 TTTTTCCTTTTTCCTTCCTT 24

RESULT 665  
BX556518  
LOCUS  
DEFINITION SALK\_139012.18.15.n Arabidopsis thaliana TDNA insertion lines  
Arabidopsis thaliana genomic clone SALK\_139012.18.15.n, genomic survey sequence.

DEFINITION BX556518 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse27g01\_plc, mRNA sequence.  
ACCESSION BX556518  
VERSION BX556518.1 GI:33427778  
KEYWORDS EST.  
SOURCE Glossina morsitans morsitans  
ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 27)

Lehane M.J., Aksoy S., Gibson W., Kerhornou A., Berriman M., Hamilton J., Soares M.B., Bonaldo M.F., Lehane S. and Hall N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942

PUBMED 14519198

COMMENT Contact: Hall N

Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix qtc are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

Location/Qualifiers

1. .27

/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse27g01\_plc"

/tissue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected gut"

/note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 19.2; DB 1; Length 27;  
Best Local Similarity 87.5%; Pred. No. 5e+02;  
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTCCTTTTCCTT 4482

Db 4 TAGAAGTTTTCCTTTTCCTT 27

RESULT 666

BX564177

LOCUS

DEFINITION BX564177 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse70b12\_plc, mRNA sequence.

ACCESSION BX564177

VERSION BX564177.1 GI:33431370

KEYWORDS EST.

SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 28)

Lehane M.J., Aksoy S., Gibson W., Kerhornou A., Berriman M., Hamilton J., Soares M.B., Bonaldo M.F., Lehane S. and Hall N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes

Genome Biol. 4 (10), R63 (2003)

```

MEDLINE
PUBMED
COMMENT
22801942
14519198
Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
FEATURES
source
Location/Qualifiers
1..28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse70b12_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/note="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.3%; Score 19.2; DB 1; Length 28;
Best Local Similarity 87.5%; Pred. No. 5.4e+02;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4482
||| ||||| ||||| ||||| |||||
DB 4 TAGAAGTTTTTTTTTTTTTTTTTTT 27

RESULT 667
A2397471
LOCUS
DEFINITION
1M0162P23F Mouse 10kb plasmid UUGCLM library Mus musculus genomic
clone UUGCLM0162P23 F, genomic survey sequence.
ACCESSION
A2397471
VERSION
A2397471.1 GI:10512543
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 32)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiser, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0162 row: P column: 23
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 32.
FEATURES
source
Location/Qualifiers
1..32
/organism="Mus musculus"
/mol_type="genomic DNA"

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/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="UUGCLM0162P23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGCLM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus CS7BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.3%; Score 19.2; DB 1; Length 32;
Best Local Similarity 75.0%; Pred. No. 7.1e+02;
Matches 24; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4012 AAAATGAGAAAAAGAGAGAAAAACAAATGTT 4043
||||| ||||| ||||| ||||| |||||
DB 1 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTT 32

RESULT 668
BQ588729/c
LOCUS
DEFINITION
S013713-024-014-B24-T7 MPZ-ADIS-024-storage root Beta vulgaris
cDNA clone 024-014-B24 3-PRIME, mRNA sequence.
ACCESSION
BQ588729
VERSION
BQ588729.1 GI:36118312
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 19)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698
Contact: Weisshaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 14 row: B column: 24
Seq primer: T7; GTAATACGACTACTATAGGC.
FEATURES
source
Location/Qualifiers
1..19
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:187281"

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/db xref="taxon:161934"
/clone="024-014-B24"
/tissue_type="storage root"
/lab_host="EMDH10B"
/clone_lib="MPI2-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4482
Db 19 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 669
LOCUS CB174047
DEFINITION OR 2032F05_010529.y1 Adult mouse olfactory epithelium library Mus
VERSION Mus musculus cDNA clone 2032F05 5', mRNA sequence.
KEYWORDS CB174047
SOURCE ESI.
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 19)
YOUNG,J.M., SHYKIND,B.M., LANE,R.P., TONNES-PRIDDY,L., ROSS,J.A.,
WALKER,M., WILLIAMS,E.M. and TRASK,B.J.
Odorant receptor expressed sequence tags demonstrate olfactory
expression of over 400 genes, extensive alternate splicing and
unequal expression levels
Genome Biol. 4 (11), R71.1-R71.15 (2003)
Contact: Young JM
Trask Lab, Division of Human Biology
Fred Hutchinson Cancer Research Center
1100 Fairview Avenue N., C3-168, P.O. Box 19024, Seattle, WA
98109-1024, USA
Tel: 206 667 1471
Fax: 206 667 6524
Email: jayoung@fhcrc.org
Seq primer: M13 Reverse.

FEATURES
source
1..19
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="2032F05"
/tissue_type="Adult"
/dev_stage="Adult"
/clone_lib="Adult mouse olfactory epithelium library"
/notes="Organ: Olfactory turbinates; Vector:
LambdaZAPII-XR; Site 1: EcoRI; Site 2: XhoI; This library
was provided by Leslie Vosshall. mRNA was prepared from
the olfactory and respiratory epithelium of an adult
mouse. Oligo-dT primed cDNA was directionally cloned into
Stratagene's lambdaZAPII-XR vector."

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4482
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 670
LOCUS CF279008
DEFINITION CF279008
19 bp mRNA linear EST 14-AUG-2003
14ETL--05-C13.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--05-C13, mRNA sequence.
ACCESSION CF279008
VERSION GI:33656394
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
KIM,J.S., JUN,K.M., CHEONG,P.J., KIM,M.J., LEE,T.H., SHIN,Y.C.,
SONG,S.I., KIM,J.K., KIM,Y.-K. and NAHM,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--05-C13"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4482
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 671
LOCUS CF291089
DEFINITION CF291089
19 bp mRNA linear EST 14-AUG-2003
14ROOT--01-G03.b1 Rice root plasmid cDNA library (14ROOT) Oryza
sativa cDNA clone 14ROOT--01-G03, mRNA sequence.
ACCESSION CF291089
VERSION GI:33660122
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 19)
KIM,J.S., JUN,K.M., CHEONG,P.J., KIM,M.J., LEE,T.H., SHIN,Y.C.,
SONG,S.I., KIM,J.K., KIM,Y.-K. and NAHM,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)

```



JOURNAL COMMENT  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

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 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 675  
 CF302327  
 LOCUS  
 DEFINITION 7LEAF--07-L24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--07-L24, mRNA sequence.

ACCESSION CF302327  
 VERSION  
 KEYWORDS EST.  
 SOURCE

ORGANISM  
 Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

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FEATURES source  
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RESULT 676

CF302456

LOCUS

DEFINITION 7LEAF--07-P22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa cDNA clone 7LEAF--07-P22, mRNA sequence.

ACCESSION CF302456

VERSION

KEYWORDS EST.  
 SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
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FEATURES source  
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RESULT 677

CF304589

LOCUS

DEFINITION ABF1--05-G10.g1 ABF3-overexpressing transgenic rice lambda phage  
 cDNA library (ABF1) Oryza sativa cDNA clone ABF1--05-G10, mRNA  
 sequence.

ACCESSION CF304589

VERSION

KEYWORDS EST.  
 SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 19)

Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,



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library (ABF) Oryza sativa cDNA clone ABF--06-L18, mRNA sequence.
ACCESSION      CF311496
VERSION        CF311496.1  GI:33683257
KEYWORDS
SOURCE
ORGANISM       Oryza sativa
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               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
JOURNAL        Unpublished (2003)
COMMENT       Contact: Nahm B.H.
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               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES             Location/Qualifiers
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                     line."

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DEFINITION    ABF--06-M03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
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ACCESSION     CF311513
VERSION       CF311513.1  GI:33683274
KEYWORDS
SOURCE        Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Query Match      0.3%; Score 19; DB 1; Length 19;
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DEFINITION    ABF--06-M03.g1 ABF3-overexpressing transgenic rice plasmid cDNA
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ACCESSION     CF311513
VERSION       CF311513.1  GI:33683274
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SOURCE        Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE      1 (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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FEATURES             Location/Qualifiers
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                     line."

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ACCESSION     CF312403
VERSION       CF312403.1  GI:33684164
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SOURCE        Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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               Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1 (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
               Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE         Large-scale Sequencing Analysis of Rice ESTs
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COMMENT       Contact: Nahm B.H.
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               Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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                     line."

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DEFINITION    ABF--08-C07.b1 ABF3-overexpressing transgenic rice plasmid cDNA
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ACCESSION     CF312403
VERSION       CF312403.1  GI:33684164
KEYWORDS
SOURCE        Oryza sativa
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE      1 (bases 1 to 19)
AUTHORS       Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
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QY      4464 TTTT TTTT TTTT TTTT TTTT 4482
Db      19 TTTT TTTT TTTT TTTT TTTT 1

RESULT 683
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DEFINITION
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VERSION   library (HD) Oryza sativa cDNA clone HD-04-C17, mRNA sequence.
KEYWORDS  EST.
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REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS   Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
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          derived from rice Histone Deacetylase overexpression
          line."

QUERY MATCH 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 TTTT TTTT TTTT TTTT TTTT 19

RESULT 684
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DEFINITION
ACCESSION CF316480 19 bp mRNA linear EST 15-AUG-2003
VERSION   library (HD) Oryza sativa cDNA clone HD-05-M14, mRNA sequence.
KEYWORDS  EST.
SOURCE    CF316480.1 GI:33688241
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
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          derived from rice Histone Deacetylase overexpression
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QUERY MATCH 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
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RESULT 684
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LOCUS   HD--05-M14, g1 OshDAC1-overexpressing transgenic rice plasmid cDNA
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ACCESSION CF316480 19 bp mRNA linear EST 15-AUG-2003
VERSION   library (HD) Oryza sativa cDNA clone HD-05-M14, mRNA sequence.
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          line."

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          line."

QUERY MATCH 0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 685
CF318788/c
LOCUS   HD--09-A23, b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION
ACCESSION CF318788 19 bp mRNA linear EST 15-AUG-2003
VERSION   library (HD) Oryza sativa cDNA clone HD-09-A23, mRNA sequence.
KEYWORDS  EST.
SOURCE    CF318788.1 GI:33690549
          Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
          1 (bases 1 to 19)
REFERENCE Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
AUTHORS   Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE     Large-scale Sequencing Analysis of Rice ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.

FEATURES
          source
          1..19
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cDNA library (HD)"
/notes=vector: PCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
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Db 19 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 686
CF329986/c
LOCUS          CF329986          19 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION    NACL--05-I09.b1 Rice callus plasmid cDNA library (NACL) Oryza
VERSION       CF329986
ACCESSION     CF329986
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
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/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
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Db 19 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 688
CF333507/c
LOCUS          CF333507          19 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION    JMT--02-G23.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--02-G23, mRNA sequence.
VERSION       CF333507
ACCESSION     CF333507
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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/lab_hosts="E.coli DH10B"
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/notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
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Db 19 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 687
CF332063
LOCUS          CF332063          19 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION    NACL--08-G19.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-G19, mRNA sequence.
VERSION       CF332063
ACCESSION     CF332063
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
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Db 19 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 687
CF332063
LOCUS          CF332063          19 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION    NACL--08-G19.g1 Rice callus plasmid cDNA library (NACL) Oryza
sativa cDNA clone NACL--08-G19, mRNA sequence.
VERSION       CF332063
ACCESSION     CF332063
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
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/organism="Oryza sativa"
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/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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SOURCE          Oryza sativa
ORGANISM        Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
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Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
      |||||
Db 19 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 688
CF333507/c
LOCUS          CF333507          19 bp  mRNA  linear  EST 18-AUG-2003
DEFINITION    JMT--02-G23.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
library (JMT) Oryza sativa cDNA clone JMT--02-G23, mRNA sequence.
VERSION       CF333507
ACCESSION     CF333507
KEYWORDS      EST.
SOURCE        Oryza sativa
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE     1 (bases 1 to 19)
AUTHORS      Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE        Large-scale Sequencing Analysis of Rice ESTs
JOURNAL      Unpublished (2003)
COMMENT      Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
1..19
/organism="Oryza sativa"
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/db_xref="taxon:4530"
/clone="NACL--08-G19"
/tissue_type="callus"
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/lab_hosts="E.coli DH10B"
/clone_lib="Rice callus plasmid cDNA library (NACL)"
/notes=vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

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University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLU, UT  
84112, USA





Plate: 0072 row: H column: 15  
 Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

Seq primer: CGTTGTAACGACGCGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

## FEATURES

Location/Qualifiers  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

source

Query Match 0.3%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482

Db 1 TTTT TTTT TTTT TTTT TTTT 19

## RESULT 696

AZ350519 19 bp DNA linear GSS 29-SEP-2000  
 LOCUS IM0088A10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0088A10 F, genomic survey sequence.

ACCESSION AZ350519.1 GI:10429756

VERSION AZ350519.1 GI:10429756

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0088 row: A column: 10

Query Match 0.3%; Score 19; DB 1; Length 19;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

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Db 1 TTTT TTTT TTTT TTTT TTTT 19

## RESULT 697

AZ364226/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0110 row: B column: 24

Seq primer: CGTTGTAACGACGCGCCAGT

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: [rdunn@genetics.utah.edu](mailto:rdunn@genetics.utah.edu)  
Insert Length: 1000 Std Error: 0.00  
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Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 19.









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Query Match      0.3%; Score 19; DB 1; Length 19;
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Db 1 TTTTTTTTTTTTTTTTTT 19
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RESULT 707
AZ441329
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE

JOURNAL
COMMENT

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19 bp DNA linear GSS 03-OCT-2000
1M0233D01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0233D01 F, genomic survey sequence.
AZ441329
AZ441329.1 GI:10565342
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD2 [G1473214]b1A129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4482
Db 19 TTTTTTTTTTTTTTTTTT 1

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LOCUS	AZ471494				
DEFINITION	1M0286E11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0286E11 F, genomic survey sequence.				
ACCESSION	AZ471494				
VERSION	AZ471494.1	GI:10629619			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 19)				

TITLE	Mouse whole genome scaffolding with paired end reads from 10xb plasmid inserts
JOURNAL	Unpublished (2000)
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA Tel: 801 585 5606 Fax: 801 585 7177 Email: ddunn@genetics.utah.edu Insert Length: 10000 Std Error: 0.00 Plate: 0286 row: E column: 11 Seq primer: CGTTGTAAACGACGCCAGT Class: plasmid ends High quality sequence stop: 19. Location/Qualifiers:
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PW042nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson

```



0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4482
      |||||
Db 1 TTTTTTTTTTTTTTTTTT 19
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RESULT 715	AZ508040/c	AZ508040	19 bp	DNA	linear	GSS 05-OCT-2000
LOCUS		1M0350B04F	Mouse	10kb	plasmid	UUGCJM library
DEFINITION		clone UUGCJM0350B04	F.	genomic	survey	sequence.

VERSION	AZ508040.1	GI:10689356
KEYWORDS	GSS.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 19)	
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.	
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb	

**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0350 row: B column: 04  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid ends  
 High quality sequence stop: 19.

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/clone="UUGC1M0350B04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42n; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA

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```

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      |||||
Db 19 TTTTTTTTTTTTTTTTTT 1

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RESULT 718
AZ585865/c      19 bp      DNA      linear      GSS 13-DEC-2000
LOCUS
DEFINITION
clone UUGC1M0391D21 F, genomic survey sequence.
ACCESSION
AZ585865
VERSION
AZ585865.1 GI:11708055
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

```

```

REFERENCE
1 (bases 1 to 19)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingley, A., von
Niederhausern, A. and Wright, D., Weiss, R.
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plasmid inserts

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JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0391 row: D column: 21
Seq primer: CTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
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0.005 inch orifice at constant velocity. The sheared DNA
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Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4482
      |||||
Db 19 TTTTTTTTTTTTTTTTTT 1

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RESULT 719
AZ593210/c      19 bp      DNA      linear      GSS 13-DEC-2000
LOCUS
DEFINITION
clone UUGC1M0404C09 R, genomic survey sequence.
ACCESSION
AZ593210
VERSION
AZ593210.1 GI:11715400
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus

```

```

REFERENCE
1 (bases 1 to 19)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, R., Stokes, R., Tingley, A., von
Niederhausern, A. and Wright, D., Weiss, R.
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plasmid inserts

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JOURNAL
Unpublished (2000)
COMMENT
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0404 row: C column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES
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/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to

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clone\_lib="Mouse 10kb plasmid UUGC1M library"  
note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male); was obtained from the Jackson  
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(<http://www.jax.org/resources/documents/dnares/>). The DNA  
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0.005 inch orifice at constant velocity. The sheared DNA  
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polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from derivative

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Query Match 0.3%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 |||||  
 Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 19

RESULT 722  
 AZ631701/c  
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 clone UUGC1M0486E01 F, genomic survey sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Stokes, R., Tingley, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
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 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0486 row: E column: 01  
 Seq primer: CGTTGTAACGACGCCAGT  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
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 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number

FEATURES  
 source  
 1..19  
 /organism="Mus musculus"  
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 /db\_xref="taxon:10090"  
 /clone="UUGC1M0486E01"  
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 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
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Query Match 0.3%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482  
 |||||  
 Db 19 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 723  
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 LOCUS  
 DEFINITION 19 bp DNA linear GSS 13-DEC-2000  
 clone UUGC1M0489H15 F, genomic survey sequence.  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus (house mouse)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Stokes, R., Tingley, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
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 plasmid inserts  
 Unpublished (2000)  
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 University of Utah  
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 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
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 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated

FEATURES  
 source  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0489H15"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated

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Query Match 0.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482  
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Db 19 TTTT TTTT TTTT TTTT TTTT 1

RESULT 724  
AZ643659/c 19 bp DNA linear GSS 14-DEC-2000  
LOCUS  
DEFINITION  
IM0507D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0507D18 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ643659.1 GI:11771446  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

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Unpublished (2000)

Contact: Robert B. Weiss

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84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0507 row: D column: 18

Seq primer: CGTTGTAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

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/clone="UUGC1M0507D18"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

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(http://www.jax.org/resources/documents/dnares/). The DNA

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inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

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and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4482  
|||||  
Db 19 TTTT TTTT TTTT TTTT TTTT 1

RESULT 725

AZ644698

LOCUS

DEFINITION

IM0508E17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

clone UUGC1M0508E17 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

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Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0508 row: E column: 17

Seq primer: CACACAGGAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1. .19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0508E17"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/notes="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

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of pWD42 [gi|4732114|gb|AF129072.1], a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to





### Query Match





Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482  
 Db 19 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 734  
 A2781876/c  
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 2M0021003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0021003 R, genomic survey sequence.  
 ACCESSION A2781876  
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 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0021 row: 0 column: 03  
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 Class: plasmid ends  
 High quality sequence stop: 19.  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482

Db 19 TTTT TTTT TTTT TTTT TTTT TTTT 1

RESULT 735  
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 VERSION A2787634.1 GI:12926621  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 19)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
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 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0034 row: M column: 12  
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 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
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 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
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 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adapted mouse DNA was annealed to  
 adapted vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.3%; Score 19; DB 1; Length 19;  
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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482

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LOCUS				
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	2M0034I24R	Mouse 10kb plasmid UUGC1M library	Mus musculus	GSS 16-FEB-2001
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ACCESSION	AZ788058			
VERSION	AZ788058			
KEYWORDS	AZ788058			
SOURCE	AZ788058	1	GI:12927475	
ORGANISM	Mus musculus	(house mouse)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	1 (bases 1 to 19)			
	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,			
	Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,			
	Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von			
	Niederhausern, A. and Wright, D., Weiss, R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb			
	plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss			
	University of Utah Genome Center			
	University of Utah			
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT			
	84112, USA			
	Tel: 801 585 5606			
	Fax: 801 585 7177			
	Email: ddunn@genetics.utah.edu			
	Insert Length: 10000	Std Error: 0.00		
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	Seq primer: CACACAGGAACAGCTATGACC			
	Class: plasmid ends			
	High quality sequence stop: 19.			
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	/clone_lib="Mouse 10kb plasmid UUGC1M library"			
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	musculus C57BL/6J (male) was obtained from the Jackson			
	Laboratory Mouse DNA Resource			
	(http://www.jax.org/resources/documents/dnares/). The DNA			
	was hydrodynamically sheared by repeated passage through a			
	0.005 inch orifice at constant velocity. The sheared DNA			
	was blunt end-repaired with T4 DNA polymerase and T4			
	polynucleotide kinase. Adaptor oligonucleotides were			
	ligated to the blunt ends in high molar excess. The			
	adapted DNA was purified and size-selected for a 9.5 to			
	10.5 kb range using preparative agarose gel			
	electrophoresis. Vector DNA was prepared from a derivative			
	of pWD42 (gi 4732114 gb AF129072.1), a copy-number			
	inducible derivative of plasmid R1. The vector was ligated			
	with adaptors complementary to the insert adaptors and			
	purified. The sheared, adapted mouse DNA was annealed to			
	adapted vector DNA, and transformed into			
	chemically-competent E. coli XL10-Gold (Stratagene) cells			
	and selected for ampicillin resistance."			
Query Match	0.3%;	Score 19;	DB 1;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;		
Matches	19;	Conservative	0;	Mismatches 0;
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LOCUS				
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VERSION	AZ789590	1	GI:12930573	
KEYWORDS	GSS.			
SOURCE	Mus musculus	(house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
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	1 (bases 1 to 19)			
	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,			
	Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,			
	Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von			
	Niederhausern, A. and Wright, D., Weiss, R.			
TITLE	Mouse whole genome scaffolding with paired end reads from 10kb			
	plasmid inserts			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Robert B. Weiss			
	University of Utah Genome Center			
	University of Utah			
	Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT			
	84112, USA			
	Tel: 801 585 5606			
	Fax: 801 585 7177			
	Email: ddunn@genetics.utah.edu			
	Insert Length: 10000	Std Error: 0.00		
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	Class: plasmid ends			
	High quality sequence stop: 19.			
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	Laboratory Mouse DNA Resource			
	(http://www.jax.org/resources/documents/dnares/). The DNA			
	was hydrodynamically sheared by repeated passage through a			
	0.005 inch orifice at constant velocity. The sheared DNA			
	was blunt end-repaired with T4 DNA polymerase and T4			
	polynucleotide kinase. Adaptor oligonucleotides were			
	ligated to the blunt ends in high molar excess. The			
	adapted DNA was purified and size-selected for a 9.5 to			
	10.5 kb range using preparative agarose gel			
	electrophoresis. Vector DNA was prepared from a derivative			
	of pWD42 (gi 4732114 gb AF129072.1), a copy-number			
	inducible derivative of plasmid R1. The vector was ligated			
	with adaptors complementary to the insert adaptors and			
	purified. The sheared, adapted mouse DNA was annealed to			
	adapted vector DNA, and transformed into			
	chemically-competent E. coli XL10-Gold (Stratagene) cells			
	and selected for ampicillin resistance."			
Query Match	0.3%;	Score 19;	DB 1;	Length 19;
Best Local Similarity	100.0%;	Pred. No. 2.4e+02;		
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DEFINITION      2M0139G08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
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VERSION          AZ841581.1  GI:13011489
KEYWORDS         GSS
SOURCE           Mus musculus (house mouse)
ORGANISM         Mus musculus
REFERENCE        1 (bases 1 to 19)
AUTHORS          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                  Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
                  Niederhausern,A. and Wright,D., Weiss,R.
TITLE            Mouse whole genome scaffolding with paired end reads from 10kb
                  plasmid inserts
JOURNAL          Unpublished (2000)
COMMENT          Contact: Robert B. Weiss
                  University of Utah Genome Center
                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                  84112, USA
                  Tel: 801 585 5606
                  Fax: 801 585 7177
                  Email: ddunn@genetics.utah.edu
                  Insert Length: 10000 Std Error: 0.00
                  Plate: 0139 row: G column: 08
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                  Class: plasmid ends
                  High quality sequence stop: 19.
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Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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adaptored DNA was purified and size-selected for a 9.5 to
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electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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RESULT 743
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LOCUS           2M0139A16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION

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VERSION          AZ841622.1  GI:13011530
KEYWORDS         GSS
SOURCE           Mus musculus (house mouse)
ORGANISM         Mus musculus
REFERENCE        1 (bases 1 to 19)
AUTHORS          Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
                  Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
                  Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
                  Niederhausern,A. and Wright,D., Weiss,R.
TITLE            Mouse whole genome scaffolding with paired end reads from 10kb
                  plasmid inserts
JOURNAL          Unpublished (2000)
COMMENT          Contact: Robert B. Weiss
                  University of Utah Genome Center
                  University of Utah
                  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                  84112, USA
                  Tel: 801 585 5606
                  Fax: 801 585 7177
                  Email: ddunn@genetics.utah.edu
                  Insert Length: 10000 Std Error: 0.00
                  Plate: 0139 row: A column: 16
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                  High quality sequence stop: 19.
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musculus C57BL/6J (male) was obtained from the Jackson
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
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polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
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10.5 kb range using preparative agarose gel
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of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
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chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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LOCUS           2M0169P10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION

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VERSION        AZ861896.1  GI:13058674
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ORGANISM       Mus musculus
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AUTHORS        Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D., Weiss,R.
TITLE          Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL        Unpublished (2000)
COMMENT        Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
               Insert Length: 10000 Std Error: 0.00
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               was hydrodynamically sheared by repeated passage through a
               0.005 inch orifice at constant velocity. The sheared DNA
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               adapted DNA was purified and size-selected for a 9.5 to
               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
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               and selected for ampicillin resistance."
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               Best Local Similarity 100.0%; Pred. No. 2.4e+02;
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RESULT 745
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LOCUS      AZ936798
DEFINITION 2M0193L10R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0193L10 R, genomic survey sequence.
ACCESSION  AZ936798

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AZ936798.1  GI:13795379
GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
               Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
               Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
               Niederhausern,A. and Wright,D., Weiss,R.
TITLE        Mouse whole genome scaffolding with paired end reads from 10kb
               plasmid inserts
JOURNAL      Unpublished (2000)
COMMENT      Contact: Robert B. Weiss
               University of Utah Genome Center
               Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
               84112, USA
               Tel: 801 585 5606
               Fax: 801 585 7177
               Email: ddunn@genetics.utah.edu
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               musculus C57BL/6J (female) was obtained from the Jackson
               Laboratory Mouse DNA Resource
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               ligated to the blunt ends in high molar excess. The
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               10.5 kb range using preparative agarose gel
               electrophoresis. Vector DNA was prepared from a derivative
               of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
               inducible derivative of plasmid R1. The vector was ligated
               with adaptors complementary to the insert adaptors and
               purified. The sheared, adapted mouse DNA was annealed to
               adapted vector DNA, and transformed into
               chemically-competent E. coli XL10-Gold (Stratagene) cells
               and selected for ampicillin resistance."
               Query Match      0.3%; Score 19; DB 1; Length 19;
               Best Local Similarity 100.0%; Pred. No. 2.4e+02;
               Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
Db      19 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 746
AZ985501/c
LOCUS      AZ985501
DEFINITION 2M0267E21F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0267E21 F, genomic survey sequence.
ACCESSION  AZ985501
VERSION    AZ985501.1  GI:13856728

```

```

KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE   1 (bases 1 to 19)
AUTHORS     Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE       Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL     Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0267 row: E column: 21
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES   Location/Qualifiers
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            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0267E21"
            /sex="Female"
            /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC2M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (female) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
            Query Match      0.3%; Score 19; DB 1; Length 19;
            Best Local Similarity 100.0%; Pred. No. 2.4e+02;
            Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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Db 19 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 747
BH000498/c BH000498
LOCUS      BH000498
DEFINITION 2M0288121F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0288121 F, genomic survey sequence.
ACCESSION  BH000498
VERSION     BH000498.1 GI:13871724
KEYWORDS    GSS.

GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 19)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0267 row: E column: 21
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES   Location/Qualifiers
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            /strain="C57BL/6J"
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            /sex="Female"
            /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
            /clone_lib="Mouse 10kb plasmid UUGC2M library"
            /note="Vector: PWD42nv; Purified genomic DNA from M.
            musculus C57BL/6J (female) was obtained from the Jackson
            Laboratory Mouse DNA Resource
            (http://www.jax.org/resources/documents/dnares/). The DNA
            was hydrodynamically sheared by repeated passage through a
            0.005 inch orifice at constant velocity. The sheared DNA
            was blunt end-repaired with T4 DNA polymerase and T4
            polynucleotide kinase. Adaptor oligonucleotides were
            ligated to the blunt ends in high molar excess. The
            adaptor DNA was purified and size-selected for a 9.5 to
            10.5 kb range using preparative agarose gel
            electrophoresis. Vector DNA was prepared from a derivative
            of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
            inducible derivative of plasmid R1. The vector was ligated
            with adaptors complementary to the insert adaptors and
            purified. The sheared, adaptor mouse DNA was annealed to
            adaptor vector DNA, and transformed into
            chemically-competent E. coli XL10-Gold (Stratagene) cells
            and selected for ampicillin resistance."
            Query Match      0.3%; Score 19; DB 1; Length 19;
            Best Local Similarity 100.0%; Pred. No. 2.4e+02;
            Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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Db 19 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 748
AL587572 LOCUS      AL587572
DEFINITION  AL587572 BP Chicken Brain Library Gallus gallus cdna clone
            ROS059B11, mRNA sequence.
ACCESSION  AL587572
VERSION     AL587572.1 GI:13192606
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)

```

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ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 20)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCTTTTGTG 4484
(*6854-1)

Seq primer: M13F.
Location/Qualifiers
1..20
/mol_type="mRNA"
/db_xref="taxon:9031"
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/dev_stage="Unknown"
/lab_host="DH10B"
/clone_lib="BP Chicken Brain Library"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dr. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCTTTTGTG 4484
(*6854-1) Poly A RNA purchased from Clontech

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4466 TTTTGTG 4484
DB 2 TTTTGTG 20

RESULT 750
LOCUS
CF282002 20 bp mRNA linear EST 14-AUG-2003
DEFINITION
14ETL--09-F01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-F01, mRNA sequence.
ACCESSION
CF282002 GI:33659389
VERSION
CF282002.1
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="14ETL--09-F01"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice etiolated leaf plasmid cDNA library
(14ETL)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4466 TTTTGTG 4484
DB 2 TTTTGTG 20

RESULT 751
LOCUS
CF282002 20 bp mRNA linear EST 14-AUG-2003
DEFINITION
14ETL--09-F01.b1 Rice etiolated leaf plasmid cDNA library (14ETL)
Oryza sativa cDNA clone 14ETL--09-F01, mRNA sequence.
ACCESSION
CF282002 GI:33659389
VERSION
CF282002.1
KEYWORDS
EST.
SOURCE
Oryza sativa
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 20)
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1..20
/mol_type="mRNA"
/cultivar="Nackdong"
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/tissue_type="leaf"
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(14ETL)"
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with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4466 TTTTGTG 4484
DB 2 TTTTGTG 20

RESULT 751
LOCUS
CF282002 20 bp mRNA linear EST 02-MAR-2001
DEFINITION
ROS061D01, mRNA sequence.
ACCESSION
AL587727 GI:13192761
VERSION
AL587727
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 20)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCTTTTGTG 4484
(*6854-1)

Seq primer: M13F.
Location/Qualifiers
1..20
/mol_type="mRNA"
/db_xref="taxon:9031"
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/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dr. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCTTTTGTG 4484
(*6854-1) Poly A RNA purchased from Clontech

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4466 TTTTGTG 4484
DB 1 TTTTGTG 19

RESULT 749
LOCUS
AL587727 20 bp mRNA linear EST 02-MAR-2001
DEFINITION
ROS061D01, mRNA sequence.
ACCESSION
AL587727 GI:13192761
VERSION
AL587727
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 20)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCTTTTGTG 4484
(*6854-1)

Seq primer: M13F.
Location/Qualifiers
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/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dr. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCTTTTGTG 4484
(*6854-1) Poly A RNA purchased from Clontech

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4466 TTTTGTG 4484
DB 1 TTTTGTG 19

RESULT 749
LOCUS
AL587727 20 bp mRNA linear EST 02-MAR-2001
DEFINITION
ROS061D01, mRNA sequence.
ACCESSION
AL587727 GI:13192761
VERSION
AL587727
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 20)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCTTTTGTG 4484
(*6854-1)

Seq primer: M13F.
Location/Qualifiers
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/mol_type="mRNA"
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/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dr. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCTTTTGTG 4484
(*6854-1) Poly A RNA purchased from Clontech

Query Match 0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4466 TTTTGTG 4484
DB 1 TTTTGTG 19

RESULT 749
LOCUS
AL587727 20 bp mRNA linear EST 02-MAR-2001
DEFINITION
ROS061D01, mRNA sequence.
ACCESSION
AL587727 GI:13192761
VERSION
AL587727
KEYWORDS
EST.
SOURCE
Gallus gallus (chicken)
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 20)
Murray, F.
BP Chicken Brain Library
Unpublished (2001)
Contact: Frazer Murray
Dept. Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
GCGGCGCTTTTGTG 4484
(*6854-1)

Seq primer: M13F.
Location/Qualifiers
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/mol_type="mRNA"
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/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
unidirectionally. Primer: Oligo dr. 5' adaptor sequence:
5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
GCGGCGCTTTTGT
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CF316662  
 LOCUS HD--06-A20.1 20 bp mRNA linear EST 15-AUG-2003  
 DEFINITION library (HD) Oryza sativa cDNA clone HD--06-A20, mRNA sequence.  
 ACCESSION CF316662  
 VERSION  
 KEYWORDS EST.  
 SOURCE GI:33688423  
 ORGANISM Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 20)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 JOURNAL  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..20  
 /organism="Oryza sativa"  
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 /cultiivar="Nackdong"  
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 /clone="HD--06-A20"  
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 /dev\_stages="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

Query Match 0.3%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4466 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT  
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RESULT 752  
 CF318278  
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 DEFINITION library (HD) Oryza sativa cDNA clone HD--08-F13, mRNA sequence.  
 ACCESSION CF318278  
 VERSION  
 KEYWORDS EST.  
 SOURCE GI:33690039  
 ORGANISM Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 20)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 JOURNAL  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.  
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 source  
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 /dev\_stages="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

Query Match 0.3%; Score 19; DB 1; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 2 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT

RESULT 753  
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 LOCUS HD--11-001.g1 20 bp mRNA linear EST 15-AUG-2003  
 DEFINITION library (HD) Oryza sativa cDNA clone HD--11-001, mRNA sequence.  
 ACCESSION CF320843  
 VERSION  
 KEYWORDS EST.  
 SOURCE GI:33692604  
 ORGANISM Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 20)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 JOURNAL  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..20  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultiivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="HD--11-001"  
 /tissue\_type="callus"  
 /dev\_stages="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDA1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

Query Match

Best Local Similarity 0.3%; Score 19; DB 1; Length 20;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

4466 TTTTCTTTTTTTTTTTTG 4484  
|||||  
2 TTTTCTTTTTTTTTTTTG 20

Db

RESULT 754

AZ341237/c

LOCUS

AZ341237

DEFINITION

IM0073G03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0073G03 R, genomic survey sequence.

ACCESSION

AZ341237

VERSION

AZ341237.1 GI:10417288

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

REFERENCE

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,W., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS

Mus whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dduun@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0073 row: G column: 03  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0073G03"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

Query Match

Best Local Similarity 0.3%; Score 19; DB 1; Length 20;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

4464 TTTTCTTTTTTTTTTTT 4482  
|||||  
19 TTTTCTTTTTTTTTTTT 1

Db

RESULT 755

AZ486784

LOCUS

AZ486784

DEFINITION

IM0315C20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0315C20 F, genomic survey sequence.

ACCESSION

AZ486784

VERSION

AZ486784.1 GI:10653898

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 20)

REFERENCE

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,W., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

AUTHORS

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dduun@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0315 row: C column: 20  
Seq primer: CGTTGTAAACGACGCCAGT  
Class: plasmid ends  
High quality sequence stop: 20.  
Location/Qualifiers  
1..20  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0315C20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

FEATURES

source

Query Match

Best Local Similarity 100.0%; Pred. No. 2.7e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```

QY      4466 TTTT...TTT 4484
Db      20 TTTT...TTT 2

RESULT 758
AZ858419/c
LOCUS    20 bp  DNA  linear  GSS 21-FEB-2001
DEFINITION  2M0163003R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
ACCESSION  AZ858419
VERSION    AZ858419.1 GI:13051545
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
REFERENCE  1 (bases 1 to 20)
AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
          Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D., Weises,R.
TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
JOURNAL   Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: dunn@genetics.utah.edu
          Insert Length: 10000 Std Error: 0.00
          Plate: 0163 row: 0 column: 03
          Seq primer: CACACAGGAAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 20.

FEATURES             source
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        /organism="Mus musculus"
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        /strain="C57BL/6J"
        /db_xref="taxon:10090"
        /clone="UUGC2M0163003"
        /sex="Male"
        /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
        /clone_lib="Mouse 10kb plasmid UUGC1M library"
        /note="Vector: pWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

Query Match      0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTT...TTT 4482

```

```

Db      20 TTTT...TTT 2

RESULT 759
AL587702
LOCUS    21 bp  mRNA  linear  EST 02-MAR-2001
DEFINITION  AL587702 BP Chicken Brain Library Gallus gallus cDNA clone
ACCESSION  ROS60609, mRNA sequence.
VERSION    AL587702
KEYWORDS  EST.
SOURCE    Gallus gallus (chicken)
ORGANISM  Gallus gallus
REFERENCE  1 (bases 1 to 21)
AUTHORS   Murray,F.
TITLE     BP Chicken Brain Library
JOURNAL   Unpublished (2001)
COMMENT   Contact: Frazer Murray
          Dept. Genomics and Bioinformatics
          Roslin Institute
          Roslin, Midlothian, EH25 9PS, UK
          Tel: +44 (0)131 527 4200
          Fax: +44 (0)131 440 0434
          Email: frazer.murray@bbsrc.ac.uk
          GCGGCGCGCTTTT...TTTTTTT 3' Poly A RNA purchased from Clontech
          (*6854-
          Seq primer: M13P.

FEATURES             source
    1. 21
        /organism="Gallus gallus"
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        /db_xref="taxon:9031"
        /clone="ROS060H09"
        /tissue_type="Brain"
        /dev_stage="Unknown"
        /lab_host="DH10B"
        /clone_lib="BP Chicken Brain Library"
        /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; Cloned
        unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
        5' TCGACCTCGAG 3' ; 3' adaptor sequence: 5'
        GCGGCGCGCTTTT...TTTTTTT 3' Poly A RNA purchased from
        Clontech (*6854-1)"

Query Match      0.3%; Score 19; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4464 TTTT...TTT 4483
Db      2 TTTT...TTT 21

RESULT 760
CF302218
LOCUS    21 bp  mRNA  linear  EST 15-AUG-2003
DEFINITION  7LEAF--07-117.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
ACCESSION  CF302218
VERSION    CF302218
KEYWORDS  EST.
SOURCE    Oryza sativa
ORGANISM  Oryza sativa
REFERENCE  1 (bases 1 to 21)
AUTHORS   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzaceae; Oryza.
          Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
          Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
          Large-scale Sequencing Analysis of Rice ESTs

Query Match      0.3%; Score 19; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4464 TTTT...TTT 4482

```

```

JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="7LEAF--07-117"
/tissue_type="leaf"
/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library II (7LEAF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

Query Match 0.3%; Score 19; DB 1; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
DB 3 TTTT TTTT TTTT TTTT TTTT TTTT 21

RESULT 761
CF314260 21 bp mRNA linear EST 15-AUG-2003
LOCUS HD--02-L11.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA
DEFINITION library (HD) Oryza sativa cDNA clone HD--02-L11, mRNA sequence.
ACCESSION CF314260
VERSION 1
KEYWORDS EST.
SOURCE GI:33686021
ORGANISM Oryza sativa
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
          Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
          Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
          Large-scale Sequencing Analysis of Rice ESTs
          Unpublished (2003)
          Contact: Nahm B.H.
          Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
          of Bioscience and Bioinformatics, Myongji University
          Yongin, Kyeonggi, Korea
          Tel: 82 31 330 6193
          Fax: 82 31 321 6355
          Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..21
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--05-C16"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.3%; Score 19; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4482
DB 22 TTTT TTTT TTTT TTTT TTTT TTTT 4

RESULT 763
AZ309907 22 bp DNA linear GSS 29-SEP-2000
LOCUS 1M0017N14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0017N14 F, genomic survey sequence.
ACCESSION AZ309907
VERSION 1
KEYWORDS GSS.
SOURCE GI:10351367
ORGANISM Mus musculus (house mouse)

```



/lab\_host="E.coli DH10B"  
/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid  
cDNA library (HD)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was  
treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
reverse transcribed and then used for PCR. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

Query Match 0.3%; Score 19; DB 1; Length 26;  
Best Local Similarity 100.0%; Pred. No. 5e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTT TTTT TTTT TTTT TTTT 4482  
|||||  
Db 8 TTTT TTTT TTTT TTTT TTTT 26

RESULT 766  
TA236D08P/c  
LOCUS  
DEFINITION T. brucei sheared genomic DNA clone 236d08, forward sequence,  
genomic survey sequence.

ACCESSION AL482943  
VERSION AL482943.1 GI:11847403  
KEYWORDS GSS.  
SOURCE Trypanosoma brucei  
ORGANISM Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma.

REFERENCE 1 (bases 1 to 26)

AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,  
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,  
Melville, S.E., Rajandream, M.A. and Barrell, B.G.

TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing  
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,  
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and  
nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR),  
Rockville, MD. Genomic DNA isolated from a cloned population of  
Trypanosoma brucei (TREU927/4 Gutat 10.1) was mechanically sheared  
to give a tight size distribution (4 kb). The v + i method used for the library construction is  
described in detail in Smith, H. and Venter, J.C. (Making small  
insert libraries for whole genome shotgun sequencing projects. In  
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.  
Barrell, Oxford University Press, 1999).

Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available  
at http://www.sanger.ac.uk/Projects/T\_brucei/.

FEATURES  
Location/Qualifiers

1..26  
/organism="Trypanosoma brucei"  
/mol\_type="genomic DNA"  
/strains="TREU927"  
/db\_xref="taxon:5691"  
/clone="236d08"

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Best Local Similarity 95.0%; Pred. No. 5e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTT TTTT TTTT TTTT TTTT 4481  
|||||  
Db 20 ATT TTTT TTTT TTTT TTTT 1

RESULT 767

BI094728

LOCUS  
DEFINITION EST-CD34N-059 cDNA library of human CD 34+ stem/progenitor cells  
Homo sapiens cDNA 3', mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BI094728.1 GI:17737109  
EST.  
Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 27)

AUTHORS Zhou, G., Chen, J., Lee, S., Terry, C., Rowley, J.D. and Wang, S.M.

TITLE The pattern of gene expression in human hematopoietic CD34+

stem/progenitor cells

UNPUBLISHED (2001)

CONTACT: Wang SM

REMARKS

University of Chicago Medical Center

5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA

TEL: 773-702-6788

FAX: 773-702-3002

EMAIL: swangl@midway.uchicago.edu

This EST fragment was amplified from cDNA Library of human CD 34+  
stem/progenitor cells with GLGI technique (Generation of Longer  
cDNA fragments from SAGE tags for Gene Identification, Proc. Natl.  
Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till  
the first CATG site of the targeted cDNA sequence.

Seq primer: M13 Forward.

Location/Qualifiers

1..27

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="Bone marrow"

/cell\_type="CD34+ stem/progenitor cells"

/clone\_lib="cDNA library of human CD 34+ stem/progenitor  
cells"

/note="3' ESTs converted from the SAGE tag sequences using  
GLGI method"

Query Match 0.3%; Score 19; DB 1; Length 27;  
Best Local Similarity 81.5%; Pred. No. 5.4e+02;  
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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|||||

Db 1 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 27

RESULT 768  
CF311022

LOCUS

DEFINITION

ABF--06-B07.g1 ABF3-overexpressing transgenic rice plasmid cDNA

library (ABF) Oryza sativa cDNA clone ABF--06-B07, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..27

source

CF311022 27 bp mRNA linear EST 15-AUG-2003  
ABF--06-B07.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
library (ABF) Oryza sativa cDNA clone ABF--06-B07, mRNA sequence.

CF311022

EST.

CF311022.1 GI:33682783

ORYZA SATIVA

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 27)

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

Location/Qualifiers

1..27

source

	/note="Vector: pT7T3D (Pharmacia) with a modified polylinker V_TYPE: phagemid; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5',
	TGTTACCAATCGAAGTGAGCGGCCGCATTTTTTTTTTTTTTTT 3'] , double-stranded cDNA was size selected, ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis lesions from one patient was kindly provided by Dr. Kevin G. Becker (NINDS/NIH)." "
	Query Match Best Local Similarity      0.3%; Score 19; DB 1; Length 27; Matches    19; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
QY	4464 TTTT***** 4482
DB	1 TTTT***** 19
RESULT 770	
TX386G03Q	27 bp DNA linear GSS 13-DEC-2000
LOCUS	T. brucei sheared genomic DNA clone 386g03, reverse sequence,
DEFINITION	genomic survey sequence.
ACCESSION	AL498287
VERSION	AL498287.1 GI:11874009
KEYWORDS	GSS.
SOURCE	Trypanosoma brucei
ORGANISM	Trypanosoma brucei
REFERENCE	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
AUTHORS	Trypanosoma. 1 (bases 1 to 27) Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE	Direct Submission
JOURNAL	Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT	Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
FEATURES	Email: nelsayed@tigr.org Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/projects/T_brucei/. Location/Qualifiers 1..27 /organism="Trypanosoma brucei" /mol_type="genomic DNA" /strain="TREU927" /db_xref="taxon:5691" /clone="386g03"
Query Match	0.3%; Score 19; DB 1; Length 27;
Best Local Similarity	100.0%; Pred. No. 5.4e+02;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	4466 TTTT*****TTTG 4484
DB	1 TTTT*****TTTG 19





[illegible]

library (ABF) Oryza sativa cDNA clone ABF--05-J14, mRNA sequence.  
 CF310757  
 VERSION CF310757.1 GI:33682518  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 29)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

# FEATURES

source  
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 /organism="Oryza sativa"  
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 /dev\_stages="14 days after germination"  
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 /clone\_lib="ABF3-overexpressing transgenic rice plasmid cDNA library (ABF)"  
 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

Query Match 0.3%; Score 19; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 6.3e+02;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4466 TTTTCTTTTCTTTTCTTTG 4484  
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 Db 29 TTTTCTTTTCTTTTCTTTG 11

RESULT 777  
 CF298427  
 LOCUS 22 bp mRNA linear EST 15-AUG-2003  
 DEFINITION 7LEAF--01-M24.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--01-M24, mRNA sequence.  
 ACCESSION CF298427  
 VERSION CF298427.1 GI:33670188  
 KEYWORDS EST.  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 22)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Query Match 0.3%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 3.7e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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# FEATURES

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 /note="Vector: PCR4-TOPO; Site\_1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.3%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 3.7e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4469 TTTTCTTTTCTTTTCTTTTGTCTGA 4490  
 |||||  
 Db 1 TTTTCTTTTCTTTTCTTTTGT 22

# RESULT 778

TA303G05P/c  
 LOCUS 22 bp DNA linear GSS 13-DEC-2000  
 DEFINITION T. brucei sheared genomic DNA clone 303g05, forward sequence, genomic survey sequence.  
 ACCESSION AL497383  
 VERSION AL497383.1 GI:11865504  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

REFERENCE 1 (bases 1 to 22)  
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R., Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L., Melville, S.E., Rajandream, M.A. and Barrell, B.G.  
 TITLE Direct Submission  
 JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
 COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
 Email: nelsayed@tigr.org  
 Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

# FEATURES

source  
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 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:5691"  
 /clone="303G05"

Query Match 0.3%; Score 18.8; DB 1; Length 22;  
 Best Local Similarity 90.9%; Pred. No. 3.7e+02;  
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 779
BX568055      23 bp mRNA linear EST 14-OCT-2003
LOCUS        morsitans morsitans adult infected gut Glossina
DEFINITION   morsitans morsitans cDNA clone Tse91f03_pic, mRNA sequence.
ACCESSION    BX568055
VERSION      BX568055.1 GI:33434952
KEYWORDS     EST.
SOURCE       Glossina morsitans morsitans
ORGANISM     Glossina morsitans morsitans
              Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
              Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
              Hippoboscidae; Glossinidae; Glossina.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
              Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
TITLE        Adult midgut expressed sequence tags from the tsetse fly Glossina
              morsitans morsitans and expression analysis of putative immune
              response genes
JOURNAL       Genome Biol. 4 (10), R63 (2003)
MEDLINE      22881942
PUBMED       14519198
COMMENT      Contact: Hall N
              Pathogen Sequencing Unit
              The Sanger Institute The Wellcome Trust Genome Campus
              Hinxton, Cambridge, CB10 1SA, UK
              Request for clones, please contact: Mike Lehane
              Prof. M.J.Lehane
              School of Biological Sciences,
              University of Wales,
              Bangor LL57 2UW
              All clones with suffix q1c are reverse primer reads starting at 5'
              end of the cDNA all pic reads are from
              the 3' end.

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                      /tissue_type="adult infected gut"
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                      gut"
                      /note="country: Zimbabwe; EST from adult gut infected with
                      T.brucei"

  Query Match          0.3%; Score 18.8; DB 1; Length 23;
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  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 780
CF290997      23 bp mRNA linear EST 14-AUG-2003
LOCUS        sativa cDNA library (14ROOT) Oryza
DEFINITION   sativa cDNA clone 14ROOT--01-E03, mRNA sequence.
ACCESSION    CF290997
VERSION      CF290997.1 GI:33660030
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

  Query Match          0.3%; Score 18.8; DB 1; Length 23;
  Best Local Similarity 90.9%; Pred. No. 4.1e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 780
CF290997      23 bp mRNA linear EST 15-AUG-2003
LOCUS        library (ABF) Oryza sativa cDNA clone ABF--06-M14, mRNA sequence.
DEFINITION   library (ABF) Oryza sativa cDNA clone ABF--06-M14, mRNA sequence.
ACCESSION    CF311534
VERSION      CF311534.1 GI:33683295
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

  Query Match          0.3%; Score 18.8; DB 1; Length 23;
  Best Local Similarity 90.9%; Pred. No. 4.1e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 4468 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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                      /clone="14ROOT--01-E03"
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                      /clone_lib="Rice root plasmid cDNA library (14ROOT)"
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                      with oligoribonucleotides and then used as templates for
                      RT-PCR."

  Query Match          0.3%; Score 18.8; DB 1; Length 23;
  Best Local Similarity 90.9%; Pred. No. 4.1e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 781
CF311534      23 bp mRNA linear EST 15-AUG-2003
LOCUS        library (ABF) Oryza sativa cDNA clone ABF--06-M14, mRNA sequence.
DEFINITION   library (ABF) Oryza sativa cDNA clone ABF--06-M14, mRNA sequence.
ACCESSION    CF311534
VERSION      CF311534.1 GI:33683295
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

  Query Match          0.3%; Score 18.8; DB 1; Length 23;
  Best Local Similarity 90.9%; Pred. No. 4.1e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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                      /tissue_type="leaf"
                      /dev_stage="14 days after germination"
                      /lab_host="E.coli DH108"
                      /clone_lib="ABF3-overexpressing transgenic rice plasmid
                      cDNA library (ABF)"
                      /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
                      for 2hrs. Oligo-capped mRNA was reverse transcribed and
                      then used for PCR. mRNA was prepared from ABA-responsive

```

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TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL         Unpublished (2003)
COMMENT         Contact: Nahm B.H.
                Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
                of Bioscience and Bioinformatics, Myongji University
                Yongin, Kyeonggi, Korea
                Tel: 82 31 330 6193
                Fax: 82 31 321 6355
                Email: bhnahm@bio.myongji.ac.kr.

FEATURES       Location/Qualifiers
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              /organism="Oryza sativa"
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              /lab_host="E.coli DH108"
              /clone_lib="Rice root plasmid cDNA library (14ROOT)"
              /note="Vector: pCR4-TOPO; Site_1: EcoRI; mRNA was capped
              with oligoribonucleotides and then used as templates for
              RT-PCR."

  Query Match          0.3%; Score 18.8; DB 1; Length 23;
  Best Local Similarity 90.9%; Pred. No. 4.1e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 4468 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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RESULT 781
CF311534      23 bp mRNA linear EST 15-AUG-2003
LOCUS        library (ABF) Oryza sativa cDNA clone ABF--06-M14, mRNA sequence.
DEFINITION   library (ABF) Oryza sativa cDNA clone ABF--06-M14, mRNA sequence.
ACCESSION    CF311534
VERSION      CF311534.1 GI:33683295
KEYWORDS     EST.
SOURCE       Oryza sativa
ORGANISM     Oryza sativa
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE    1 (bases 1 to 23)
AUTHORS      Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
              Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

  Query Match          0.3%; Score 18.8; DB 1; Length 23;
  Best Local Similarity 90.9%; Pred. No. 4.1e+02;
  Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

  QY 4468 TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
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FEATURES       Location/Qualifiers
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              /mol_type="mRNA"
              /cultivar="Nackdong"
              /db_xref="taxon:4530"
              /clone="ABF--06-M14"
              /tissue_type="leaf"
              /dev_stage="14 days after germination"
              /lab_host="E.coli DH108"
              /clone_lib="ABF3-overexpressing transgenic rice plasmid
              cDNA library (ABF)"
              /note="Vector: pCR4-TOPO; Site_1: EcoRI; Leaf was dried
              for 2hrs. Oligo-capped mRNA was reverse transcribed and
              then used for PCR. mRNA was prepared from ABA-responsive

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and selected for ampicillin resistance."

Query Match	0.3%;	Score 18.8;	DB 1;	Length 23;
Best Local Similarity	90.9%;	Pred. No. 4.1e+02;		
Matches 20;	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;

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RESULT 783
AZ486853
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

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AZ486853 23 bp DNA linear GSS 05-OCT-2000  
 1M0315M14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0315M14 R, genomic survey sequence.  
 AZ486853  
 AZ486853.1 GI:10654033  
 GSS.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 23)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, N., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0315 row: M column: 14  
 Seq primer: CACACAGGAGACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 23.

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FEATURES
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high quality sequence scop: 23.
location/Qualifiers
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/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: pPW42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (GI|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

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Query Match          0.3%; Score 18.8; DB 1; Length 23;
Best Local Similarity 90.9%; Pred. No. 4.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTTCCTTTTTCCTTTTGT 4485
      ||||| ||||| ||||| |||||
Db 1 TTTTTCCTTTTTCCTTTTTCCTTTT 22

RESULT 784
AZ627841
LOCUS
DEFINITION
  1M0474E01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
  clone UUGC1M0474E01 F, genomic survey sequence.
ACCESSION
  AZ627841
VERSION
  AZ627841.1 GI:11750127
KEYWORDS
  GSS.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 23)
REFERENCE
  1 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
    Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
    Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
    Niederhausern,A. and Wright,D., Weiss,R.
  Mouse whole genome scaffolding with paired end reads from 10kb
  plasmid inserts
  Unpublished (2000)
JOURNAL
  Contact: Robert B. Weiss
COMMENT
  University of Utah Genome Center
  University of Utah
  Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
  84112, USA
  Tel: 801 585 5606
  Fax: 801 585 7177
  Email: ddunn@genetics.utah.edu
  Insert Length: 10000 Std Error: 0.00
  Plate: 0474 row: E column: 01
  Seq primer: CGTTGTAACGACGCGCCAGT
  Class: plasmid ends
  High quality sequence stop: 23.
  Location/Qualifiers
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      /organism="Mus musculus"
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      /strain="C57BL/6J"
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      /clone="UUGC1M0474E01"
      /sex="Male"
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      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

FEATURES
  source
    1..23
      /organism="Mus musculus"
      /mol_type="genomic DNA"
      /strain="C57BL/6J"
      /db_xref="taxon:10090"
      /clone="UUGC1M0474E01"
      /sex="Male"
      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
      /clone_lib="Mouse 10kb plasmid UUGC1M library"
      /notes="Vector: PWD42nv; Purified genomic DNA from M.
        musculus C57BL/6J (male) was obtained from the Jackson
        Laboratory Mouse DNA Resource
        (http://www.jax.org/resources/documents/dnares/). The DNA
        was hydrodynamically sheared by repeated passage through a
        0.005 inch orifice at constant velocity. The sheared DNA
        was blunt end-repaired with T4 DNA polymerase and T4
        polynucleotide kinase. Adaptor oligonucleotides were
        ligated to the blunt ends in high molar excess. The
        adaptor DNA was purified and size-selected for a 9.5 to
        10.5 kb range using preparative agarose gel
        electrophoresis. Vector DNA was prepared from a derivative
        of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
        inducible derivative of plasmid R1. The vector was ligated
        with adaptors complementary to the insert adaptors and
        purified. The sheared, adaptor mouse DNA was annealed to
        adaptor vector DNA, and transformed into
        chemically-competent E. coli XL10-Gold (Stratagene) cells
        and selected for ampicillin resistance."

Query Match          0.3%; Score 18.8; DB 1; Length 23;

```



**TITLE** Adult midgut expressed sequence tags from the tsetse fly *Glossina morsitans morsitans* and expression analysis of putative immune response genes

**JOURNAL** Genome Biol. 4 (10), R63 (2003)

**MEDLINE** 22881942

**PUBMED** 14519198

**COMMENT** Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehané  
Prof. M.J. Lehané  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

**FEATURES** source

1. .27  
Location/Qualifiers  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse1909.pic"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected gut"  
/notes="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 18.8; DB 1; Length 27;  
Best Local Similarity 90.9%; Pred. No. 5.8e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 4460 GGACTTTTTTTTTTTTTTTTTTTT 4481  
|||||  
**Db** 6 GGTGCTTTTTTTTTTTTTTTTTTTT 27

**RESULT 789**  
**TA247F06P/c**  
**LOCUS** TA247F06P 30 bp DNA linear GSS 13-DEC-2000  
**DEFINITION** T. brucei sheared genomic DNA clone 247f06, forward sequence, genomic survey sequence.  
**ACCESSION** AL483252  
**VERSION** AL483252.1 GI:11848928  
**KEYWORDS** GSS.  
**SOURCE** Trypanosoma brucei  
**ORGANISM** Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
1 (bases 1 to 30)  
Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R., Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L., Melville S.E., Rajandream M.A. and Barrell B.G.  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

**TITLE** moritans morsitans and expression analysis of putative immune response genes

**JOURNAL** Genome Biol. 4 (10), R63 (2003)

**MEDLINE** 22881942

**PUBMED** 14519198

**COMMENT** Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehané  
Prof. M.J. Lehané  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all pic reads are from the 3' end.

**FEATURES** source

1. .27  
Location/Qualifiers  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
/db\_xref="taxon:37546"  
/clone="Tse1909.pic"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected gut"  
/notes="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.3%; Score 18.8; DB 1; Length 27;  
Best Local Similarity 90.9%; Pred. No. 5.8e+02;  
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**QY** 4460 GGACTTTTTTTTTTTTTTTTTTTT 4481  
|||||  
**Db** 6 GGTGCTTTTTTTTTTTTTTTTTTTT 27

**RESULT 789**  
**TA247F06P/c**  
**LOCUS** TA247F06P 30 bp DNA linear GSS 13-DEC-2000  
**DEFINITION** T. brucei sheared genomic DNA clone 247f06, forward sequence, genomic survey sequence.  
**ACCESSION** AL483252  
**VERSION** AL483252.1 GI:11848928  
**KEYWORDS** GSS.  
**SOURCE** Trypanosoma brucei  
**ORGANISM** Trypanosoma brucei  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.  
1 (bases 1 to 30)  
Hall N., Bowman S., Lennard N.J., Doggett J., Atkin R., Chillingworth C., Ormond D., Harris B., El-Sayed N., Hou L., Melville S.E., Rajandream M.A. and Barrell B.G.  
Direct Submission  
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk  
Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
Email: nelsayed@tigr.org  
Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

**FEATURES** source

1. .30  
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/mol\_type="genomic DNA"  
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/db\_xref="taxon:5691"  
/clone="247f06"

Query Match 0.3%; Score 18.8; DB 1; Length 30;  
Best Local Similarity 76.7%; Pred. No. 7.3e+02;  
Matches 23; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

**QY** 4018 AGAAAAAGAGAGAAAAACAAATGTTATTT 4047  
|||||  
**Db** 30 AAAAAAAGAAAAAATTTTTTTT 1

**RESULT 790**  
**AA912788/c**  
**LOCUS** AA912788 25 bp mRNA linear EST 14-APR-1998  
**DEFINITION** ol31c03.81 Soares NFL T.GBC.S1.Homo sapiens cDNA clone IMAGE:1525060 3' similar to SW:YA2C\_SCHPO\_Q09703 HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME 1 PRECURSOR.; mRNA sequence.  
**ACCESSION** AA912788  
**VERSION** AA912788.1 GI:3052180  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 25)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LML; contact the IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.  
Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
**FEATURES** Location/Qualifiers  
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/clone="IMAGE:1525060"  
/lab\_host="DH10B"  
/clone\_lib="Soares NFL T.GBC.S1"  
/notes="Organ: pooled; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site: 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI CGAP GCBI) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

Query Match 0.2%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; Pred. No. 5.3e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

**QY** 4463 CTTTTTTTTTTTTTTTTTTTGTCT 4487  
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**Db** 25 CTTTTTCTATTGTTTGAT 1

**RESULT 791**





Plate: 0234 row: H column: 18  
Seq primer: CACACAGGAAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 25.

**FEATURES**  
**source**

1. 25  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0234H18"  
/sex="Male"  
/lab\_host="E. Coli strain Xu10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 [Gil14732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli Xu10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; Pred. No. 5.3e+02;

QY	4464	TTTTTTTTTTTTTTTTTTTTTTTGTCTT	4488
Db	25	TTTTTTTTTTTTTTTTTTAAATTTTTTTTTT	1

RESULT 794

Accession	LOCUS	AZ476141	25 bp	DNA	linear	GSS 04-OCT-2000
AB0001759	DEFINITION	Mouse 10kb plasmid UGCLM library				Mus musculus genomic
		clone UGCLM0294M10 R.				genomic survey sequence.

ACCESSION	AZ476141
VERSION	AZ476141.1
GI	10634266

KEYWORDS  
SOURCE  
GSS.  
Mus musculus (house mouse)

ORGANISM	Mus musculus
REFERENCE	1 (bases 1 to 25)
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

**AUTHORS**

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D. Weiss, R.

**TITLE**  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
Unpublished (2000)

COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah Cancer  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

**Fax: 801 585 7177**

Email: [ddunn@genetics.utah.edu](mailto:ddunn@genetics.utah.edu)

Insert Length: 10000 Std Error: 0.00

plate: 0294 row: M column: 10

Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 25.

**FEATURES**  
**SOURCE**

1. 25

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUCG1M0294M10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_libs="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
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electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1|, a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

Query Match 0.2%; Score 18.6; DB 1; Length 25;  
Best Local Similarity 84.0%; pred. No. 5.3e+02;

QY	4465	TTTTTTTTTTTTTTTTTTGCTTG	4489
Db	1	TTTTTTTTTTTTTTTTTTGCTTG	25

## RESULT 795

LOCUS	25 bp	DNA	linear	GSS
BZ765670	SALK_133356.14.20.x	Arabidopsis thaliana	TDNA insertion lines	GSS 13-MAR-2003
DEFINITION	Arabidopsis thaliana genomic clone SALK_133356.14.20.x, genomic survey sequence.			

ACCESSION BZ765670

ACCESSION  
VERSION  
KEYWORDS

KEYWORDS	SOURCE	ORGANISM	GENUS	SPECIES	COLLECTOR	DATE	LOCALITY	ALTITUDE	ECOSYSTEM	THREATS	STATUS	REMARKS
Arabidopsis thaliana (thale cress)	Arabidopsis thaliana	Arabidopsis thaliana	Arabidopsis	thaliana								

ORGANISM

*Arabiopsis thaliana*  
Eukaryota; Viridiplantae  
Eukaryota; Streptophyta; Embryophyta; Tracheophyta;  
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
1 (bases 1 to 25)

REFERENCE

REFERENCE  
AUTHORS  
ALONGO, J. M. LEIS  
I (BASES I CO 23

**AUTHORS**  
ARONSON, J. M., BELTSKE, I. J., BARAJAS, F., CHEN, N., CHEUK, K.,  
GADRINAB, C., JESKE, A., KARNES, M., KIM, C. J., PARKER, H., P.  
SHINN, P., ZIMMERMAN, J. and ECKER, J. R.

**TITLE**  
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
Shinn, P., Zimmerman, J. and Ecker, J.R.

Arabisopsis Genome  
Published (2001)

Journal of Management Inquiry 20(1) 2011

COMMENT  
Contact: Joseph R. Ecker  
Cell: Treatments Genetic Analysis Laboratory (CICN21)

Salk Institute Genomic Analysis Laboratory

The Salk Institute for Biological Studies  
10018 V. Tennen, Pines Road, La Jolla, CA 92037 USA

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel.: 858 452 4100 x1752

Tel: 858 453 4100

**Fax: 858 558 6379**

Email: ecker@salk.edu  
This is single pass sequence recovered from the left border of  
TDNA.

IDNA:  
Class: TDNA tagged.

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FEATURES
source
  Location/Qualifiers
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      /note="PCR was performed on Arabidopsis thaliana lines
      each of which contains one or more TDNA insertion
      elements. The resultant fragment for each line was
      directly sequenced to determine the genomic sequence at
      the site of insertion. Details of the protocols used can
      be found at http://signal.salk.edu/tdna_protocols.html"
      0.2%; Score 18.6; DB 1; Length 25;
      Best Local Similarity 84.0%; Pred. No. 5.3e+02;
      Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4461 GACATTTTCTTTTCTTTTCTTTTCT 4485
Db 1 GATTTTCTTTTCTTTTCTTTTCT 25

RESULT 796
BM658913
LOCUS
DEFINITION
  LOG602768282.R1 CSEQFXL36 fetal brain Sus scrofa CDNA, mRNA
  26 bp mRNA linear EST 27-FEB-2002
  sequence.
ACCESSION
  BM658913
VERSION
  BM658913.1 GI:18959184
KEYWORDS
  EST.
SOURCE
  Sus scrofa (pig)
  Sus scrofa
  ORGANISM
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
  1 (bases 1 to 26)
  Adelson, D.L. and Gill, C.A.
  Porcine ESTs
  Unpublished (2002)
  Contact: David L. Adelson
  Animal Breeding and Genetics
  Texas A&M University
  Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
  USA
  Tel.: 9798452616
  Fax: 9798456970
  Email: david.adelson@tamu.edu.
  Location/Qualifiers
    1..26
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      /db_xref="taxon:9823"
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      (5'-NNN_NNNinsert)
      CGGAATGGAGCTCACCGCGTGGCGCGCGCTCGAG. Sequence 3' of
      the inserts (AAGATTCGATCAAGCTTATCGATACCGTCGACCTCGAG.
      non-normalized library, sequenced 3' with M13R primer."
      0.2%; Score 18.6; DB 1; Length 26;
      Best Local Similarity 84.0%; Pred. No. 5.8e+02;
      Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTTCTTTTCT 4488
Db 1 TTTTCTTTTCTTTTCTTTTCTTTTCT 25

RESULT 797
BX563414
LOCUS
DEFINITION
  BX563414 Glossina morsitans morsitans adult infected gut Glossina
  morsitans morsitans CDNA clone Tse66e05_p1c, mRNA sequence.
  26 bp mRNA linear EST 10-OCT-2003
  Glossina morsitans morsitans
  ORGANISM
    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
    Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
    Hippoboscidae; Glossinidae; Glossina.
    1 (bases 1 to 26)
    Lehane, M.J., Akcoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
    Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
    Adult midgut expressed sequence tags from the tsetse fly Glossina
    morsitans morsitans and expression analysis of putative immune
    response genes
    Genome Biol. 4 (10), R63 (2003)
    22881942
    14519198
    Contact: Hall N
    Pathogen Sequencing Unit
    The Sanger Institute The Wellcome Trust Genome Campus
    Hinxton, Cambridge, CB10 1SA, UK
    Request for clones, please contact: Mike Lehane
    Prof. M.J. Lehane
    School of Biological Sciences,
    University of Wales,
    Bangor LL57 2UW
    All clones with suffix q1c are reverse primer reads starting at 5'
    end of the cDNA all p1c reads are from
    the 3' end.
    Location/Qualifiers
      1..26
        /organism="Glossina morsitans morsitans"
        /mol_type="mRNA"
        /sub_species="morsitans"
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        /clone="Tse66e05_p1c"
        /tissue_type="adult infected gut"
        /clone_lib="Glossina morsitans morsitans adult infected
        gut"
        /note="country: Zimbabwe; EST from adult gut infected with
        T.brucei"
      0.2%; Score 18.6; DB 1; Length 26;
      Best Local Similarity 84.0%; Pred. No. 5.8e+02;
      Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4464 TTTTCTTTTCTTTTCTTTTCTTTTCT 4488
Db 1 TTTTCTTTTCTTTTCTTTTCTTTTCT 25

RESULT 798
CF337311
LOCUS
DEFINITION
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  library (JMT) Oryza sativa cDNA clone JMT--07-L06, mRNA sequence.
  26 bp mRNA linear EST 18-AUG-2003
  CF337311
  VERSION
  CF337311.1 GI:33823014
  KEYWORDS
  EST.
  SOURCE
  Oryza sativa
  ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
    1 (bases 1 to 26)
    Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
    Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
    Large-scale Sequencing Analysis of Rice ESTs
    Unpublished (2003)
    Contact: Nahm B.H.

```



/clone\_lib="Mouse 10kb plasmid UGCM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 18.6; DB 1; Length 26;  
 Best Local Similarity 84.0%; Pred. No. 5.8e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4465 TTTTCTTTTCTTTTCTTTGCTTG 4489  
 ||||| ||||| ||||| ||||| |||||  
 Db 2 TTTTCTTTTCTTTTCTTTGCTTG 26

## RESULT 801

BZ593276  
 LOCUS SALK\_068322.21.25.n Arabidopsis thaliana DNA insertion lines  
 DEFINITION Arabidopsis thaliana genomic clone SALK\_068322.21.25.n, genomic survey sequence.

ACCESSION BZ593276  
 VERSION BZ593276.1 GI:27533795  
 KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 26)  
 AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J., and Ecker, J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the

Arabidopsis Genome

UNPUBLISHED (2001)

CONTACT: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: ecker@alk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

source

1. .26

/organism="Arabidopsis thaliana"

/mol\_type="genomic DNA"

/strain="Columbia 0"

/db\_xref="taxon:3702"

/clone="SALK\_068322.21.25.n"

/clone\_lib="Arabidopsis thaliana TDNA insertion lines"  
 /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can be found at [http://signal.salk.edu/tdna\\_protocols.html](http://signal.salk.edu/tdna_protocols.html)"

Query Match 0.2%; Score 18.6; DB 1; Length 26;  
 Best Local Similarity 84.0%; Pred. No. 5.8e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4461 GACTTTTTTTTTTTTTTTTTTTTGT 4485  
 ||||| ||||| ||||| ||||| |||||  
 Db 2 GAGTTTTTTTTTTTCTTTTCTTTT 26

## RESULT 802

CF318113/c

LOCUS

DEFINITION

HD--08-B07\_g1 OshDAC1-overexpressing transgenic rice plasmid cDNA

library (HD) Oryza sativa clone HD--08-B07, mRNA sequence.

ACCESSION CF318113

VERSION CF318113.1 GI:33698974

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 27)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

UNPUBLISHED (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Gyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

Location/Qualifiers

1. .27

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="HD--08-B07"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_host="E.coli DH10B"

/clone\_lib="OshDAC1-overexpressing transgenic rice plasmid

cDNA library (HD)"

/note="Vector: pCR4-TOPO; Site 1: EcoRI; Callus was

treated with ABA(20um) for 1hr. Oligo-capped mRNA was

reverse transcribed and then used for PCR. mRNA was

derived from rice Histone Deacetylase overexpression

line."

Query Match 0.2%; Score 18.6; DB 1; Length 27;

Best Local Similarity 84.0%; Pred. No. 6.3e+02;

Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTCTTTTCTTTTCTTTTGT 4488

||||| ||||| ||||| ||||| |||||

Db 27 TTTTCTTTTCTTTTCTTTTCTTTTGT 3

## RESULT 803

AZ495352

LOCUS

DEFINITION

1M0331E14F Mouse 10kb plasmid UGCM library Mus musculus genomic

clone UGCM1M0331E14 F, genomic survey sequence.

ACCESSION AZ495352

VERSION AZ495352.1 GI:10670743

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

AZ495352  
 1M0331E14F Mouse 10kb plasmid UGCM library Mus musculus genomic  
 clone UGCM1M0331E14 F, genomic survey sequence.

ACCESSION AZ495352  
 VERSION AZ495352.1 GI:10670743  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)



QY 4459- TGGACTTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483





ACCESSION	EX552134	
VERSION	EX552134.1	GI:33376432
KEYWORDS	EST.	
SOURCE	Glossina morsitans morsitans	

MEDLINE	22881942	Contact: Hall N	Pathogen Sequencing Unit	The Wellcome Trust Genome Campus
PUBMED	14519198		The Sanger Institute	Hinxton, Cambridge, CB10 1SA, UK
COMMENT				

Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all p1c reads are from  
 the 3' end.

#### FEATURES

source  
 1. .28  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tsei27b06\_p1c"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected  
 gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;  
 Best Local Similarity 84.0%; Pred. No. 6.8e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

#### RESULT 814

LOCUS BX553346 28 bp mRNA linear EST 10-OCT-2003  
 DEFINITION BX553346 Glossina morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone Tsei28h02\_p1c, mRNA sequence.

ACCESSION BX553346.1 GI:33377521

VERSION BX553346

KEYWORDS EST.

SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 28)

AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,  
 Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942

PUBMED 14519198

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all p1c reads are from

the 3' end.

#### FEATURES

source  
 1. .28  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tsei28h02\_p1c"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected

Gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;  
 Best Local Similarity 84.0%; Pred. No. 6.8e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

#### RESULT 815

LOCUS BX553393

DEFINITION BX553393 Glossina morsitans morsitans adult infected gut Glossina  
 morsitans morsitans cDNA clone Tsei29b11\_p1c, mRNA sequence.

ACCESSION BX553393

VERSION BX553393.1 GI:33377563

KEYWORDS EST.

SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (bases 1 to 28)

AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,

Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina  
 morsitans morsitans and expression analysis of putative immune  
 response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942

PUBMED 14519198

COMMENT

Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'  
 end of the cDNA all p1c reads are from  
 the 3' end.

#### FEATURES

source  
 1. .28  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tsei29b11\_p1c"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected  
 gut"  
 /note="country: Zimbabwe; EST from adult gut infected with  
 T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;  
 Best Local Similarity 84.0%; Pred. No. 6.8e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

#### RESULT 816

LOCUS BX553451

DEFINITION BX553451 Glossina morsitans morsitans adult infected gut Glossina

morsitans morsitans cDNA clone Tse129e08\_plc, mRNA sequence.  
 BX553451  
 VERSION BX553451.1 GI:33377612  
 EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 28)  
 REFERENCE Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 AUTHORS Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
 source  
 1..28  
 Location/Qualifiers  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse129e08\_plc"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;  
 Best Local Similarity 84.0%; Pred. No. 6.8e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483  
 ||| |||||  
 Db 4 TAGATAGTTTTTTTTTTTTTTTTTT 28

RESULT 817  
 BX553531  
 LOCUS BX553531 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse12a08\_plc, mRNA sequence.  
 DEFINITION  
 ACCESSION BX553531 GI:33377683  
 VERSION BX553531  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 28)  
 REFERENCE Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 AUTHORS Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942

14519198  
 PUBMED  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
 source  
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 Location/Qualifiers  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"  
 /sub\_species="morsitans"  
 /db\_xref="taxon:37546"  
 /clone="Tse12a08\_plc"  
 /tissue\_type="adult infected gut"  
 /clone\_lib="Glossina morsitans morsitans adult infected gut"  
 /note="country: Zimbabwe; EST from adult gut infected with T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;  
 Best Local Similarity 84.0%; Pred. No. 6.8e+02;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483  
 ||| |||||  
 Db 4 TAGATAGTTTTTTTTTTTTTTTTTT 28

RESULT 818  
 BX553626  
 LOCUS BX553626 Glossina morsitans morsitans adult infected gut Glossina morsitans morsitans cDNA clone Tse12f05\_plc, mRNA sequence.  
 DEFINITION  
 ACCESSION BX553626 GI:33377771  
 VERSION BX553626  
 KEYWORDS EST.  
 SOURCE Glossina morsitans morsitans  
 ORGANISM Glossina morsitans morsitans  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Hippoboscidae; Glossinidae; Glossina.  
 1 (bases 1 to 28)  
 REFERENCE Lehane, M.J., Aksoy, S., Gibson, W., Keshornou, A., Berriman, M., Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
 AUTHORS Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
 TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina morsitans morsitans and expression analysis of putative immune response genes  
 JOURNAL Genome Biol. 4 (10), R63 (2003)  
 MEDLINE 22881942  
 PUBMED 14519198  
 COMMENT Contact: Hall N  
 Pathogen Sequencing Unit  
 The Sanger Institute The Wellcome Trust Genome Campus  
 Hinxton, Cambridge, CB10 1SA, UK  
 Request for clones, please contact: Mike Lehane  
 Prof. M.J. Lehane  
 School of Biological Sciences,  
 University of Wales,  
 Bangor LL57 2UW  
 All clones with suffix q1c are reverse primer reads starting at 5' end of the cDNA all plc reads are from the 3' end.

FEATURES  
 source  
 1..28  
 Location/Qualifiers  
 /organism="Glossina morsitans morsitans"  
 /mol\_type="mRNA"





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QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 824
BX555683
LOCUS BX555683 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse22b11_pic, mRNA sequence.
ACCESSION BX555683
VERSION BX555683.1 GI:33379660
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 28)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
FEATURES
source
1. .28
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse22d02_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 826
BX555881
LOCUS BX555881 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse23e03_pic, mRNA sequence.
ACCESSION BX555881
VERSION BX555881.1 GI:33379851
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 28)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
```

```
REFERENCE
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE 22881942
PUBMED 14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.
FEATURES
source
1. .28
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse22d02_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"
Query Match 0.2%; Score 18.6; DB 1; Length 28;
Best Local Similarity 84.0%; Pred. No. 6.8e+02;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483
Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

RESULT 826
BX555881
LOCUS BX555881 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION morsitans morsitans cDNA clone Tse23e03_pic, mRNA sequence.
ACCESSION BX555881
VERSION BX555881.1 GI:33379851
KEYWORDS EST.
SOURCE Glossina morsitans morsitans
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 28)
Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
```











[illegible][illegible]

Bangor LL57 20W  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

## FEATURES

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Location/Qualifiers

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/mol\_type="mRNA"  
/sub\_species="morsitans"  
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/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

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Best Local Similarity 84.0%; Pred. No. 6.8e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

## RESULT 840

BX560221

LOCUS

DEFINITION BX560221 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse48g03\_plc, mRNA sequence.

ACCESSION

BX560221

VERSION

BX560221.1

KEYWORDS

SOURCE

ORGANISM

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE

AUTHORS

Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 20W  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

## FEATURES

source

Location/Qualifiers

1. .28  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
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/clone="Tse48g03\_plc"  
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/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;  
Best Local Similarity 84.0%; Pred. No. 6.8e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

## RESULT 841

BX562150

LOCUS

DEFINITION BX562150 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse5a06\_plc, mRNA sequence.

ACCESSION

BX562150

VERSION

BX562150.1

KEYWORDS

SOURCE

ORGANISM

Glossina morsitans morsitans  
Glossina morsitans morsitans  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Hippoboscoidae; Glossinidae; Glossina.

REFERENCE

AUTHORS

Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,  
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.  
Adult midgut expressed sequence tags from the tsetse fly Glossina  
morsitans morsitans and expression analysis of putative immune  
response genes

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J. Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 20W  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

## FEATURES

source

Location/Qualifiers

1. .28  
/organism="Glossina morsitans morsitans"  
/mol\_type="mRNA"  
/sub\_species="morsitans"  
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/clone="Tse5a06\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe; EST from adult gut infected with  
T.brucei"

Query Match 0.2%; Score 18.6; DB 1; Length 28;  
Best Local Similarity 84.0%; Pred. No. 6.8e+02;  
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4459 TGGACTTTTTTTTTTTTTTTTTTTT 4483

Db 4 TAGATAGTTTTTTTTTTTTTTTTTTT 28

## RESULT 842

BX562296

LOCUS

DEFINITION BX562296 Glossina morsitans morsitans adult infected gut Glossina  
morsitans morsitans cDNA clone Tse5h05\_plc, mRNA sequence.

ACCESSION

BX562296

VERSION

BX562296.1

KEYWORDS





Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnamgghio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source

Location/Qualifiers

1. .20

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="ABF-03-A01"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid

cDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site\_1: EcoRI; Leaf was dried  
for 2hrs. Oligo-capped mRNA was reverse transcribed and  
then used for PCR. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

Query Match 0.2%; Score 18.4; DB 1; Length 20;  
Best Local Similarity 95.0%; Pred. No. 3.5e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4464 TTTTGTGTTTTTTTTTTT 4483

Db 1 TTTTGTGTTTTTTTTTTT 20

## RESULT 848

A2375620/c

LOCUS

DEFINITION A2375620 20 bp DNA linear GSS 02-OCT-2000  
IM0129A08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0129A08 F, genomic survey sequence.

ACCESSION

A2375620

VERSION

A2375620.1

GI:10489320

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0129 row: A column: 08

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

1. .20

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0129A08"

/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## Query Match

Best Local Similarity

0.2%; Score 18.4; DB 1; Length 20;

Matches 19; Conservative

0; Mismatches 1; Indels

0; Gaps

QY 4464 TTTTGTGTTTTTTTTTTT 4483

Db 20 TTTTGTGTTTTTTTTTTT 1

## RESULT 849

A2486787

LOCUS

DEFINITION

A2486787

VERSION

A2486787.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 20)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0315 row: D column: 23

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 20.

Location/Qualifiers

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0315D23"

/sex="Male"





musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD2 [G1473214|G51AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

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Query Match      0.2%;   Score 18.4;   DB 1;   Length 20;
Best Local Similarity 95.0%;   Pred. No. 3.5e+02;
Matches 19;   Conservative 0;   Mismatches 1;   Indels 0;   Gaps 0;

Qy  4464  TTTTTTTTTTTTTTTTTT 4483
Db    20  TTTTTTTTTTTTTTTTTT 1

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[illegible]

14319198  
Contact: Hall N  
Pathogen Sequencing Unit  
The Sanger Institute The Wellcome Trust Genome Campus  
Hinxton, Cambridge, CB10 1SA, UK  
Request for clones, please contact: Mike Lehane  
Prof. M.J.Lehane  
School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5',  
end of the cDNA all p1c reads are from the 3' end

```

FEATURES
source
Location/Qualifiers
1..21
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse101g03_p1c"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
note="country: Zimbabwe; EST from adult gut infected with

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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
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/clone="UUC1M0012H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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      ||||| ||||| ||||| |||||
Db 2 CTTTTTTTTTTTTTTTTTTT 21

RESULT 857
AZ317208
LOCUS      21 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION  LM003502R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M003502 R, genomic survey sequence.
ACCESSION  AZ317208
VERSION    A2317208.1 GI:10365804
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE   1 (bases 1 to 21)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: J column: 02
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
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/mol_type="genomic DNA"

/organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0012H15"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4463 CTTTTTTTTTTTTTTTTTTT 4482
      ||||| ||||| ||||| |||||
Db 2 CTTTTTTTTTTTTTTTTTTT 21

RESULT 857
AZ317208
LOCUS      21 bp      DNA      linear      GSS 29-SEP-2000
DEFINITION  LM003502R Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M003502 R, genomic survey sequence.
ACCESSION  AZ317208
VERSION    A2317208.1 GI:10365804
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE   1 (bases 1 to 21)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0035 row: J column: 02
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 21.
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/mol_type="genomic DNA"

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/clone_lib="Mouse 10kb plasmid UUC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match      0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTTTT 4483
      ||||| ||||| ||||| |||||
Db 1 TTTTTTTTTTTTTTTTTTTT 20

RESULT 858
AZ486776
LOCUS      21 bp      DNA      linear      GSS 05-OCT-2000
DEFINITION  LM003510P Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M003510 F, genomic survey sequence.
ACCESSION  AZ486776
VERSION    A2486776.1 GI:10653882
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE   1 (bases 1 to 21)
AUTHORS    Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL    Unpublished (2000)
COMMENT    Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0315 row: M column: 10
Seq primer: CGTTGTAACACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 21.
Location/Qualifiers
1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"

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/clone="UUGC2M0156D09"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

```

Query Match      0.2%; Score 18.4; DB 1; Length 21;
Best Local Similarity 95.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
      ||||| ||||| ||||| ||||| ||||| |||||
Db 21 TTTT TTTT GTTTTT TTTT TTTT TTTT TTTT 2

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RESULT 861
BX556059      22 bp mRNA linear EST 10-OCT-2003
LOCUS      BX556059 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION      morsitans morsitans CDNA clone Tse24f09_p1c, mRNA sequence.
ACCESSION      BX556059
VERSION      BX556059.1 GI:33380008
KEYWORDS      EST.
SOURCE      Glossina morsitans morsitans
ORGANISM      Glossina morsitans morsitans

```

```

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 22)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198

```

```

COMMENT      Contact: Hall N
              The Sanger Sequencing Unit
              Hinxton, Cambridge, CB10 1SA, UK
              Request for clones, please contact: Mike Lehane
              Prof. M.J. Lehane
              School of Biological Sciences,
              University of Wales,
              Bangor LL57 2UW

```

```

All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
FEATURES
source
1..22
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"

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/clone="Tse24f09_p1c"
/tissue type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

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Query Match      0.2%; Score 18.4; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 4.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
      ||||| ||||| ||||| ||||| ||||| |||||
Db 2 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 21

```

```

RESULT 862
BX590647      23 bp mRNA linear EST 06-DEC-2002
LOCUS      S015086-024-018-P17-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
DEFINITION      cDNA clone 024-018-P17 5-PRIME, mRNA sequence.
ACCESSION      BX590647
VERSION      BX590647.1 GI:26120230
KEYWORDS      EST.
SOURCE      Beta vulgaris
ORGANISM      Beta vulgaris

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 23)
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
12472698

```

```

COMMENT      Contact: Weisshaar B
              ADIS DNA core facility at MP1Z
              Max-Planck-Institute for Plant Breeding Research
              Carl-von-Linne Weg 10, 50829 Koeln, Germany
              Fax: 00492215062851
              Email: weisshaar@mpiz-koeln.mpg.de
              Insert Length: 23 Std Error: 0.00
              Plate: 18 row: P column: 17
              Seq primer: SP6; CATACGATTTAGTGACACTATAG.
              Location/Qualifiers
              1..23
              /organism="Beta vulgaris"
              /mol_type="mRNA"
              /cultivar="KWS2320 (double haploid, monogerm breeding
              line)"
              /db_xref="GABI:189468"
              /db_xref="taxon:161934"
              /clone="024-018-P17"
              /tissue type="storage root"
              /lab host="EMDH10B"
              /clone_lib="MP1Z-ADIS-024-storage root"
              /notes="Vector: PCWVSPORT6; Site 1: Sali; Site 2: NotI;
              cDNA library from sugar beet, library provided by KWS
              Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
              b.schulz@kwa.de; cloning sites Sali-NotI, primer sites and
              orientation:
              SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
              Sequencing granted in the context of the GABI-Beet
              project, local PI: Dr. Katharina Schneider, coordinator:
              Prof. Christian Jung; Sequence submission managed by
              RZPD/GABI-Primary database: http://gabi.rzpd.de"

```

```

Query Match      0.2%; Score 18.4; DB 1; Length 23;
Best Local Similarity 95.0%; Pred. No. 4.8e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 4464 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 4483
      ||||| ||||| ||||| ||||| ||||| |||||
Db 2 TTTT TTTT TTTT TTTT TTTT TTTT TTTT 21

```

```

RESULT 861
BX556059      22 bp mRNA linear EST 10-OCT-2003
LOCUS      BX556059 Glossina morsitans morsitans adult infected gut Glossina
DEFINITION      morsitans morsitans CDNA clone Tse24f09_p1c, mRNA sequence.
ACCESSION      BX556059
VERSION      BX556059.1 GI:33380008
KEYWORDS      EST.
SOURCE      Glossina morsitans morsitans
ORGANISM      Glossina morsitans morsitans

```

```

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
1 (bases 1 to 22)
Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,
Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.
Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
Genome Biol. 4 (10), R63 (2003)
22881942
14519198

```

```

COMMENT      Contact: Hall N
              The Sanger Sequencing Unit
              Hinxton, Cambridge, CB10 1SA, UK
              Request for clones, please contact: Mike Lehane
              Prof. M.J. Lehane
              School of Biological Sciences,
              University of Wales,
              Bangor LL57 2UW

```

```

All clones with suffix q1c are reverse primer reads starting at 5'
end of the cDNA all p1c reads are from
the 3' end.
FEATURES
source
1..22
Location/Qualifiers
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"

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4463 CTTTCTTTTCTTTTCTTTT 4482  
 Db 2 CTTTCTTTTCTTTTCTTTT 21

RESULT 863  
 CF290998/c  
 LOCUS 23 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 14ROOT--01-E03.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
 sativa cDNA clone 14ROOT--01-E03, mRNA sequence.  
 CF290998  
 VERSION  
 ACCESSION  
 SOURCE  
 ORGANISM  
 Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 1 (bases 1 to 23)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..23  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="14ROOT--01-E03"  
 /tissue\_type="root"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice root plasmid cDNA library (14ROOT)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 18.4; DB 1; Length 23;  
 Best Local Similarity 95.0%; Pred. No. 4.8e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

4466 TTTTCTTTTCTTTTCTTTTGT 4485  
 Db 1 TTTTCTTTTCTTTTCTTTTGT 20

RESULT 865  
 CF314322  
 LOCUS 23 bp mRNA linear EST 15-AUG-2003  
 DEFINITION HD--02-M20.g1 OSHDAC1-overexpressing transgenic rice plasmid cDNA  
 library (HD) Oryza sativa cDNA clone HD--02-M20, mRNA sequence.  
 CF314322  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 1 (bases 1 to 23)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 CONTACT: Nahm B.H.  
 GENOMICS AND GENETICS INSTITUTE, GREENGENE BIOTECH INC.; DIVISION  
 OF BIOSCIENCE AND BIOINFORMATICS, MYONGJI UNIVERSITY  
 YONGIN, KYEONGGI, KOREA  
 TEL: 82 31 330 6193  
 FAX: 82 31 321 6355  
 EMAIL: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
 source  
 1..23  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="HD--02-M20"  
 /tissue\_type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="OSHDAC1-overexpressing transgenic rice plasmid  
 cDNA library (HD)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was  
 treated with ABA(20um) for 1hr. Oligo-capped mRNA was  
 reverse transcribed and then used for PCR. mRNA was  
 derived from rice Histone Deacetylase overexpression  
 line."

4468 TTTTCTTTTCTTTTCTTTTGTCT 4487  
 Db 23 TTTTCTTTTCTTTTCTTTTGTCT 4

RESULT 864  
 CF291486  
 LOCUS 23 bp mRNA linear EST 14-AUG-2003  
 DEFINITION 14ROOT--01-021.b1 Rice root plasmid cDNA library (14ROOT) Oryza  
 sativa cDNA clone 14ROOT--01-021, mRNA sequence.  
 CF291486  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Oryza sativa  
 Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.  
 1 (bases 1 to 23)  
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

Query Match 0.2%; Score 18.4; DB 1; Length 23;  
 Best Local Similarity 95.0%; Pred. No. 4.8e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

REFERENCE  
AUTHORS

Query Match 0.2%; Score 18.4; DB 1; Length 23;  
Best Local Similarity 95.0%; Pred. No. 4.8e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483  
| | | | | | | | | | | | | | | | | | | | | |  
DB 1 TTTT TTTT TTTT TTTT TTTT TTTT 20

## RESULT 866

CF333801  
LOCUS  
DEFINITION JMT--02-N11.g1 AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT) Oryza sativa cDNA clone JMT--02-N11, mRNA sequence.

ACCESSION CF333801  
VERSION  
KEYWORDS EST.  
SOURCE CF333801.1 GI:333815910  
ORGANISM Oryza sativa

## REFERENCE

1 (bases 1 to 23)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

## AUTHORS

Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)

## TITLE

## JOURNAL

## COMMENT

Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongui University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

## source

1..23  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="JMT--02-N11"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="AtJMT-overexpressing transgenic rice plasmid cDNA library (JMT)"  
/note="vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from Arabidopsis Jasmonate Carboxyl methyltransferase overexpression line."

Query Match 0.2%; Score 18.4; DB 1; Length 23;  
Best Local Similarity 95.0%; Pred. No. 4.8e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4483  
| | | | | | | | | | | | | | | | | | | | | |  
DB 2 TGT TTTT TTTT TTTT TTTT TTTT 21

## RESULT 867

AZ627850/c  
LOCUS  
DEFINITION IM0474N20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0474N20 F, genomic survey sequence.

ACCESSION AZ627850  
VERSION  
KEYWORDS GSS.  
SOURCE AZ627850.1 GI:11750136  
ORGANISM Mus musculus (house mouse)

## REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS

1 (bases 1 to 24)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
Unpublished (2000)

## TITLE

## JOURNAL

## COMMENT

Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0474 row: N column: 20

Seq primer: CGTTGTAAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 24.

## FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0474N20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 18.4; DB 1; Length 24;  
Best Local Similarity 95.0%; Pred. No. 5.3e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4463 CTTT TTTT TTTT TTTT TTTT TTTT 4482  
| | | | | | | | | | | | | | | | | | | | | |  
DB 20 CTTT TTTT TTTT TTTT TTTT TTTT 1

## RESULT 868

## LOCUS

AZ764519/c  
DEFINITION IM0560P11R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0560P11 R, genomic survey sequence.

ACCESSION AZ764519

VERSION AZ764519.1 GI:12879566

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 24)

**AUTHORS** Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  
**TITLE** Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0560 row: P column: 11  
 Seq primer: CACACAGGAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 24.  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCIM0560P11"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGCIM library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

**Query Match** 0.2%; Score 18.4; DB 1; Length 24;  
**Best Local Similarity** 95.0%; Pred. No. 5.3e+02;  
**Matches** 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 4462 ACTTTTTTTTTTTTTTTT 4481  
 20 AATTTTTTTTTTTTTTTT 1

**Db**

**RESULT 869**  
**AW333508**  
**LOCUS** AW333508 26 bp mRNA linear EST 31-JAN-2000  
**DEFINITION** S22F8 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence.  
**ACCESSION** AW333508  
**VERSION** AW333508.1 GI:68229865  
**KEYWORDS** EST.  
**SOURCE** Pneumocystis carinii  
**ORGANISM** Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes; Pneumocystidaceae; Pneumocystis.  
**REFERENCE** 1 (bases 1 to 26)  
**AUTHORS** Smullan,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C., Edman,J.C., Kovacs,J. and Cushion,M.

**Expressed sequence tags from Pneumocystis carinii**  
 Unpublished (2000)  
 Contact: Staben C  
 School of Biological Sciences  
 University of Kentucky  
 101 Morgan Building, University of Kentucky, Lexington, KY 40506-0225, USA  
 Tel: 606 257 2161  
 Fax: 606 257 1717  
 Email: staben@pop.uky.edu.  
 Location/Qualifiers  
 1. 26  
 /organism="Pneumocystis carinii"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4754"  
 /lab\_host="E. coli"  
 /clone\_lib="AGS-1"  
 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI; P. carinii organisms (3x10e9) from a single rat [99-1-6, sacrificed on 3/17/99] at Cincinnati VA facilities. Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/project/Pneumocystis/"

**Query Match** 0.2%; Score 18.4; DB 1; Length 26;  
**Best Local Similarity** 95.0%; Pred. No. 6.3e+02;  
**Matches** 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 4464 TTTTTTTTTTTTTTTT 4483  
 1 TTTTTTTTTTTTTTTT 20

**Db**

**RESULT 870**  
**CF315308**  
**LOCUS** CF315308 27 bp mRNA linear EST 15-AUG-2003  
**DEFINITION** HD--04-C22.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--04-C22, mRNA sequence.  
**ACCESSION** CF315308  
**VERSION** CF315308.1 GI:33687069  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
**REFERENCE** 1 (bases 1 to 27)  
**AUTHORS** Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1. 27  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="HD--04-C22"  
 /tissue type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was

**TITLE** JOURNAL COMMENT  
 Expressed sequence tags from Pneumocystis carinii  
 Unpublished (2000)  
 Contact: Staben C  
 School of Biological Sciences  
 University of Kentucky  
 101 Morgan Building, University of Kentucky, Lexington, KY 40506-0225, USA  
 Tel: 606 257 2161  
 Fax: 606 257 1717  
 Email: staben@pop.uky.edu.  
 Location/Qualifiers  
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 /organism="Pneumocystis carinii"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4754"  
 /lab\_host="E. coli"  
 /clone\_lib="AGS-1"  
 /note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI; P. carinii organisms (3x10e9) from a single rat [99-1-6, sacrificed on 3/17/99] at Cincinnati VA facilities. Trizol extracted RNA. Oligo dT priming, standard conditions described by vendor, Stratagene. Further details see www.uky.edu/project/Pneumocystis/"

**FEATURES**  
 source

**Query Match** 0.2%; Score 18.4; DB 1; Length 26;  
**Best Local Similarity** 95.0%; Pred. No. 6.3e+02;  
**Matches** 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**QY** 4464 TTTTTTTTTTTTTTTT 4483  
 1 TTTTTTTTTTTTTTTT 20

**RESULT 870**  
**CF315308**  
**LOCUS** CF315308 27 bp mRNA linear EST 15-AUG-2003  
**DEFINITION** HD--04-C22.g1 OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD) Oryza sativa cDNA clone HD--04-C22, mRNA sequence.  
**ACCESSION** CF315308  
**VERSION** CF315308.1 GI:33687069  
**KEYWORDS** EST.  
**SOURCE** Oryza sativa  
**ORGANISM** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.  
**REFERENCE** 1 (bases 1 to 27)  
**AUTHORS** Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
 Location/Qualifiers  
 1. 27  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="HD--04-C22"  
 /tissue type="callus"  
 /dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="OshDAC1-overexpressing transgenic rice plasmid cDNA library (HD)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; Callus was treated with ABA(20um) for 1hr. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was

**FEATURES**  
 source



derived from rice Histone Deacetylase overexpression line."

Query Match 0.2%; Score 18.4; DB 1; Length 27;  
 Best Local Similarity 95.0%; Pred. No. 6.8e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 4467 TTTTTCCTTTTTCCTTC 4486  
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 Db 1 TTTTTCCTTTTTCCTTC 20

RESULT 871  
 AZ514352/c  
 LOCUS  
 DEFINITION 28 bp DNA linear GSS 05-OCT-2000  
 clone UUGC1M0360F06 R, genomic survey sequence.  
 ACCESSION AZ514352  
 VERSION AZ514352.1 GI:10695668  
 GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (Bases 1 to 28)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.,  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0360 row: F column: 06  
 Seq primer: CACACAGGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0360F06"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel,  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 18.4; DB 1; Length 28;  
 Best Local Similarity 78.6%; Pred. No. 7.3e+02;  
 Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
 QY 4012 AAAATGAGAAAAAGAGAGAAAAA 4039  
 |||||  
 Db 28 AAAAAGAAAAA 1  
 RESULT 872  
 AZ357605  
 LOCUS  
 DEFINITION 28 bp DNA linear GSS 02-OCT-2000  
 clone UUGC1M0099115 F, genomic survey sequence.  
 ACCESSION AZ357605  
 VERSION AZ357605.1 GI:10471305  
 GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (Bases 1 to 28)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.,  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0099 row: I column: 15  
 Seq primer: CGTGTAAACGACGCGCAGT  
 Class: plasmid ends  
 High quality sequence stop: 28.  
 Location/Qualifiers  
 1..28  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0099115"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

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Query Match      0.2%; Score 18.4; DB 1; Length 28;
Best Local Similarity 78.6%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4020 AAAAAAGAGAGAAACAAATGTTATTT 4047
      ||||| 1 ||||| ||||| ||||| |||||
Db 1 AAAAAAAAAAAAAAAAAATTTTTTTT 28

RESULT 873
CF307749/c
LOCUS
DEFINITION ABF--01-E17.b1 ABF3-overexpressing transgenic rice plasmid cDNA
Library (ABF) Oryza sativa cDNA clone ABF--01-E17, mRNA sequence.
ACCESSION CF307749
VERSION
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 28)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnam@gbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
source
Location/Qualifiers
1..28
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="ABF--01-E17"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="ABF3-overexpressing transgenic rice plasmid
cDNA library (ABF)"
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; Leaf was dried
for 2hrs. Oligo-capped mRNA was reverse transcribed and
then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match      0.2%; Score 18.4; DB 1; Length 28;
Best Local Similarity 78.6%; Pred. No. 7.3e+02;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAA 4039
      ||||| 1 ||||| ||||| ||||| |||||
Db 28 AAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 874
BX556035
LOCUS
DEFINITION BX556035 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse24e05_pic, mRNA sequence.
ACCESSION BX556035
VERSION
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Query Match      0.2%; Score 18.4; DB 1; Length 28;
Best Local Similarity 95.0%; Pred. No. 7.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTTTTTTTTTTTTTTTTT 4481
      | ||||| ||||| ||||| |||||
Db 9 AGTTTTTTTTTTTTTTTTTTT 28

RESULT 875
BX560649
LOCUS
DEFINITION BX560649 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse50c12_pic, mRNA sequence.
ACCESSION BX560649
VERSION
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE
PUBMED
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane

```

```

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE
PUBMED
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane
School of Biological Sciences,
University of Wales,
Bangor LL57 2UW
All clones with suffix qic are reverse primer reads starting at 5'
end of the cDNA all pic reads are from
the 3' end.

FEATURES
source
Location/Qualifiers
1..28
/organism="Glossina morsitans morsitans"
/mol_type="mRNA"
/sub_species="morsitans"
/db_xref="taxon:37546"
/clone="Tse24e05_pic"
/tissue_type="adult infected gut"
/clone_lib="Glossina morsitans morsitans adult infected
gut"
/notes="country: Zimbabwe; EST from adult gut infected with
T.brucei"

Query Match      0.2%; Score 18.4; DB 1; Length 28;
Best Local Similarity 95.0%; Pred. No. 7.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTTTTTTTTTTTTTTTTT 4481
      | ||||| ||||| ||||| |||||
Db 9 AGTTTTTTTTTTTTTTTTTTT 28

RESULT 875
BX560649
LOCUS
DEFINITION BX560649 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse50c12_pic, mRNA sequence.
ACCESSION BX560649
VERSION
KEYWORDS
SOURCE
ORGANISM Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Hippoboscoidae; Glossinidae; Glossina.
REFERENCE 1 (bases 1 to 28)
AUTHORS Lehane,M.J., Aksoy,S., Gibson,W., Kerhornou,A., Berriman,M.,
Hamilton,J., Soares,M.B., Bonaldo,M.F., Lehane,S. and Hall,N.
TITLE Adult midgut expressed sequence tags from the tsetse fly Glossina
morsitans morsitans and expression analysis of putative immune
response genes
JOURNAL Genome Biol. 4 (10), R63 (2003)
MEDLINE
PUBMED
COMMENT Contact: Hall N
Pathogen Sequencing Unit
The Sanger Institute The Wellcome Trust Genome Campus
Hinxton, Cambridge, CB10 1SA, UK
Request for clones, please contact: Mike Lehane
Prof. M.J.Lehane

```

School of Biological Sciences,  
University of Wales,  
Bangor LL57 2UW  
All clones with suffix q1c are reverse primer reads starting at 5'  
end of the cDNA all plc reads are from  
the 3' end.

## FEATURES

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Location/Qualifiers  
/organism="Glossina morsitans morsitans"  
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/clone="rse50c12\_plc"  
/tissue\_type="adult infected gut"  
/clone\_lib="Glossina morsitans morsitans adult infected  
gut"  
/note="country: Zimbabwe, EST from adult gut infected with  
T.brucei"

Query Match 0.2%; Score 18.4; DB 1; Length 28;  
Best Local Similarity 95.0%; Pred. No. 7.3e+02;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4462 ACTTTTCTTTTCTTTTCTTTT 4481

Db 9 AGTTTTTTTTTTTTTTTTTT 28

RESULT 876  
A2785111/c  
LOCUS A2785111 31 bp DNA linear GSS 16-FEB-2001  
DEFINITION 2M002B14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC2M002B14 R, genomic survey sequence.

ACCESSION A2785111

VERSION A2785111.1 GI:12921525

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

## REFERENCE

AUTHORS 1 (bases 1 to 31)  
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

## JOURNAL

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0028 row: B column: 14

Seq primer: CACACAGGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 31.

## FEATURES

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/sex="Male"

/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 18.4; DB 1; Length 31;  
Best Local Similarity 78.6%; Pred. No. 8.9e+02;  
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAACAAAA 4039

Db 30 AAAAAAAAAAAAAAAAAAGAAAAAAAAA 3

RESULT 877

AZ307192

LOCUS

DEFINITION

clone UUGC1M000807 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

REFERENCE

AUTHORS

1 (bases 1 to 34)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,

Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,

Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von

Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

plasmid inserts

JOURNAL

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0008 row: B column: 07

Seq primer: CACACAGGAACACGTATGACC

Class: plasmid ends

High quality sequence stop: 34.

source  
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/strain="C57BL/6J"

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/clone="UUGC1M000807"

/sex="Male"

/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 18.4; DB 1; Length 34;  
Best Local Similarity 78.6%; Pred. No. 1e+03; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 6;

QY 4012 AAATGAGAAAAAGAGAAAAACAAA 4039  
|||||  
Db 6 AAAAAAGAAAAA

RESULT 878  
CF297907 23 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF-01-B05.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF-01-B05, mRNA sequence.

ACCESSION CF297907  
VERSION CF297907.1 GI:33669668  
KEYWORDS EST.

SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 23)  
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355

Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES

source

1..23  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF-01-B05"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 18.2; DB 1; Length 23;  
Best Local Similarity 87.0%; Pred. No. 5.2e+02; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 3;

QY 4466 TTTTCTTTTCTTTTCTTTTCTTT 4488  
|||||  
Db 1 TTTTCTTTTCTTTTCTTTTCTTT 23

RESULT 879  
CF291636

LOCUS

DEFINITION

CF291636

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 24)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.  
Location/Qualifiers

FEATURES

source

1..24

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="14ROOT-02-C09"

/tissue\_type="root"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice root plasmid cDNA library (14ROOT)"

/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 18.2; DB 1; Length 24;  
Best Local Similarity 87.0%; Pred. No. 5.7e+02; Indels 0; Gaps 0;  
Matches 20; Conservative 0; Mismatches 3;

QY 60 CGGAGGCTCGGGGGCGGGCGG 82

|||||

Db 2 CGGCGGGCGGGCGGGCGGGCGG 24

RESULT 880  
CF337747

LOCUS

DEFINITION

CF337747

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 24)

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C., Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.

TITLE Large-scale Sequencing Analysis of Rice ESTs

JOURNAL Unpublished (2003)

COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea

FEATURES

source

1..24

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4530"

/clone="14ROOT-02-C09"

/tissue\_type="root"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="Rice root plasmid cDNA library (14ROOT)"

/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

## FEATURES

## source

1. 24  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="JMT-08-P05"  
 /tissue\_type="leaf"  
 /dev\_stage="14 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="AclJMT-overexpressing transgenic rice plasmid  
 cDNA library (JMT)"  
 /note="Vector: pCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA  
 was reverse transcribed and then used for PCR. mRNA was  
 prepared from Arabidopsis Jaemoinate Carboxyl  
 methyltransferase overexpression line."

Query Match 0.2%; Score 18.2; DB 1; Length 24;  
 Best Local Similarity 87.0%; Pred. No. 5.7e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4469 TTTTCTTTTCTTTGCTTGTGAG 4491  
 |||||  
 Db 1 TTTTCTTTTCTTTGCTTGTATAG 23

## RESULT 881

## LOCUS

DEFINITION T57657 25 bp mRNA linear EST 08-FEB-1995  
 IMAGE:75507 3' similar to similar to gb:M17589 TYROSINE  
 3-MONOOXYGENASE ISOZYMES (HUMAN), mRNA sequence.

ACCESSION T57657.1 GI:659518

VERSION T57657.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (Bases 1 to 25)

## AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
 Chiesse, S., Dietrich, N., Dubucque, T., Favello, A., Gish, W.,  
 Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,  
 Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,  
 Rohlfing, T., Scheillenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J.,  
 Travaekis, E., Underwood, K., Wohlmann, P., Waterston, R., Wilson, R.  
 and Marra, M.

TITLE Generation and analysis of 280,000 human expressed sequence tags

JOURNAL Genome Res. 6 (9), 807-828 (1996)

MEDLINE 9704478

PUBMED 8889549

COMMENT Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Trace considered overall poor quality

Seq primer: -21m13

High quality sequence stop: 1.

Location/Qualifiers

1. 25

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:505236"

/db\_xref="taxon:9606"  
 /clone="IMAGE:75507"  
 /sex="female"  
 /dev\_stage="49 year old"  
 /lab\_host="SOUR cells (kanamycin resistant)"  
 /clone\_lib="Stratagene ovary (#937217)"  
 /note="Organ: ovary; Vector: Bluescript SK; Site 1: EcoRI;  
 Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dT.  
 Total ovary tissue, normal, caucasian. Average insert  
 size: 0.8 kb; Uni-ZAP XR Vector: -5' adaptor sequence: 5'  
 GAATTCGGCAGGAG 3' -3' adaptor sequence: 5'  
 CTCGAGTGTCTTTTCTTTT 3'"

Query Match 0.2%; Score 18.2; DB 1; Length 25;  
 Best Local Similarity 87.0%; Pred. No. 6.2e+02;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4471 TTTTCTTTTCTTTGCTTGTGAGAC 4493  
 |||||  
 Db 1 TTTTCTTTTCTTTTGTAGAC 23

## RESULT 882

## LOCUS

DEFINITION BX560008 26 bp mRNA linear EST 10-OCT-2003  
 morsitans morsitans cDNA clone Tse47c08\_p1c, mRNA sequence.

ACCESSION BX560008

VERSION BX560008.1 GI:33368000

KEYWORDS EST.

SOURCE Glossina morsitans morsitans

ORGANISM Glossina morsitans morsitans

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Hippoboscidae; Glossinidae; Glossina.

REFERENCE 1 (Bases 1 to 26)

AUTHORS Lehane, M.J., Aksoy, S., Gibson, W., Kerhornou, A., Berriman, M.,

Hamilton, J., Soares, M.B., Bonaldo, M.F., Lehane, S. and Hall, N.

Adult midgut expressed sequence tags from the tsetse fly Glossina

morsitans morsitans and expression analysis of putative immune

response genes

JOURNAL Genome Biol. 4 (10), R63 (2003)

MEDLINE 22881942

PUBMED 14519198

COMMENT Contact: Hall N

Pathogen Sequencing Unit

The Sanger Institute The Wellcome Trust Genome Campus

Hinxton, Cambridge, CB10 1SA, UK

Request for clones, please contact: Mike Lehane

Prof. M.J. Lehane

School of Biological Sciences,

University of Wales,

Bangor LL57 2UW

All clones with suffix q1c are reverse primer reads starting at 5'

end of the cDNA all p1c reads are from

the 3' end.

## FEATURES

## source

1. 26

/organism="Glossina morsitans morsitans"

/mol\_type="mRNA"

/sub\_species="morsitans"

/db\_xref="taxon:37546"

/clone="Tse47c08\_p1c"

/tissue\_type="adult infected gut"

/clone\_lib="Glossina morsitans morsitans adult infected

gut"

/note="country: Zimbabwe; EST from adult gut infected with

T.brucei"

## FEATURES

## source

1. 25

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="GDB:505236"

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

```

QY 4459 TGGACTTTTTTTTTTTTTTTT 4481
| | | | | | | | | | | | | | | | | |
Db 4 TAGAAGTTTTTTTTTTTTTTTTT 26

RESULT 883
AZ785554/c 27 bp DNA linear GSS 16-FEB-2001
LOCUS 2M0029G02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0029G02 R, genomic survey sequence.
ACCESSION AZ785554
VERSION AZ785554.1 GI:12922429
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 27)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0029 row: G column: 02
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 27.

FEATURES
source
1. 27
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0029G02"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

Query Match 0.2%; Score 18.2; DB 1; Length 27;
Best Local Similarity 87.0%; Pred. No. 7.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4464 TTTTITTTTTTTTTTTTTTTC 4486

```

```

Db 26 TTTTITGTTTTTTTTC 4

RESULT 884
AU013658/c 33 bp mRNA linear EST 03-AUG-1998
LOCUS AU013658 Schizosaccharomyces pombe late log phase cDNA
DEFINITION Schizosaccharomyces pombe cDNA clone spc08464, mRNA sequence.
ACCESSION AU013658
VERSION AU013658.1 GI:3368449
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
1 (bases 1 to 33)
AUTHORS Morimyo,M. and Mita,K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces
pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-Chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.

FEATURES
Location/Qualifiers
source
1. 33
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc08464"
/sex="h minus"
/notes="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"

Query Match 0.2%; Score 18.2; DB 1; Length 33;
Best Local Similarity 74.2%; Pred. No. 1e+03;
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4009 TCTAAATGAGAAAAAGAGAGACAAAA 4039
| | | | | | | | | | | | | | | | | |
Db 32 TTTAAAAAAGAAAAAGAAAAAGAAAAA 2

RESULT 885
AV743346
LOCUS AV743346 CB Homo sapiens cDNA clone CEWAED12 5', mRNA sequence.
DEFINITION AV743346
ACCESSION AV743346
VERSION AV743346.1 GI:10860927
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 33)
AUTHORS Zhang,Q., Ye,M., Wu,X., Gu,J., Huang,Q., Zhou,J., Shen,Y., Han,Z.,
Chen,S., Mao,M. and Chen,Z.
TITLE Homo sapiens CB library cDNA clones
JOURNAL Unpublished (2000)
COMMENT Contact: Zhu Chen
Shanghai Institute of Hematology, Rui-Jin Hospital
197 Rui-Jin II Road, Shanghai 200025, P. R. China
Tel: 86-21-64740490
Fax: 86-21-64743206

```

Email: mbshi@ms.stn.sh.cn  
This clone is available at Shanghai Hematology Institute in Shanghai.  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.  
Location/Qualifiers

# FEATURES

1..33  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CBMABD12"  
/tissue\_type="cord blood"  
/cell\_type="CD34+ hematopoietic stem/progenitor cell"  
/lab\_host="BM25.8"  
/clone\_lib="CB"  
/note="Vector: pBluescript; Site 1: EcoRI; The insert is cloned randomly with the EcoRI digestion"

Query Match 0.2%; Score 18.2; DB 1; Length 33;  
Best Local Similarity 69.7%; Pred. No. 1e+03;  
Matches 23; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 4007 GCTCTAAATGAGAAAAAGAGAGACAAACAAA 4039  
|||||  
Db 1 GCCCNAAAAAAGAAAAAAGAAAAAAGAAAAA 33

RESULT 886  
AW334249/C  
LOCUS  
DEFINITION S32D4 AGS-1 Pneumocystis carinii cDNA 3', mRNA sequence. EST 31-JAN-2000  
ACCESSION AW334249  
VERSION AW334249.1 GI:6830606  
KEYWORDS EST.  
SOURCE Pneumocystis carinii  
ORGANISM Pneumocystis carinii

REFERENCE  
AUTHORS Eukaryota; Fungi; Ascomycota; Pneumocystidomycetes;  
Pneumocystidaceae; Pneumocystis.  
1 (bases 1 to 34)  
AUTHORS Smilian,A.G., Arnold,J., Weise,M., Wunderlich,J., Staben,C.,  
Edman,J.C., Kovacs,J. and Cushion,M.

TITLE Expressed sequence tags from Pneumocystis carinii  
JOURNAL Unpublished (2000)  
COMMENT Contact: Staben C  
School of Biological Sciences  
University of Kentucky  
101 Morgan Building, University of Kentucky, Lexington, KY  
40506-0225, USA  
Tel: 606 257 2161  
Fax: 606 257 1717  
Email: staben@pop.uky.edu.

FEATURES  
source  
1..34  
/organism="Pneumocystis carinii"  
/mol\_type="mRNA"  
/db\_xref="taxon:4754"  
/lab\_host="E. coli"  
/clone\_lib="AGS-1"  
/note="Vector: Lambda ZAP II; Site 1: EcoRI; Site 2: XhoI;  
P. carinii organisms (3x10e9) from a single rat (99-1-6,  
sacrificed on 3/17/99) at Cincinnati VA facilities.  
Trizol extracted RNA. Oligo dt priming, standard  
conditions described by vendor, Stratagene. Further  
details see www.uky.edu/Project/Pneumocystis/"

Query Match 0.2%; Score 18.2; DB 1; Length 34;  
Best Local Similarity 74.2%; Pred. No. 1.1e+03;  
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4009 TCTAAATGAGAAAAAGAGACAAACAAA 4039  
|||||  
Db 33 TTTAAAAAAGAAAAAAGAAAAAAGAAAAA 3

# RESULT 887

AW345610  
LOCUS

DEFINITION 1M080C24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M080C24 F, genomic survey sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AW345610  
GSS.  
Mus musculus (house mouse)

REFERENCE  
AUTHORS

1 (bases 1 to 34)  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00  
Plate: 0080 row: C column: 24  
Seq primer: CGTTGTAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 34.

FEATURES  
source  
1..34  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M080C24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, TI-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid RI. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 18.2; DB 1; Length 34;  
Best Local Similarity 74.2%; Pred. No. 1.1e+03;  
Matches 23; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4009 TCTAAATGAGAAAAAGAGACAAACAAA 4039  
|||||  
Db 1 TTTAAAAAAGAAAAAAGAAAAAAGAAAAA 31





of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

# FEATURES

source  
1. .18  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/culturivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="14ETL--03-J04"  
/tissue\_type="leaf"  
/dev\_stages="14 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice etiolated leaf plasmid cDNA library (14ETL)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4481  
|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 18

RESULT 891  
CF297446 18 bp mRNA linear EST 14-AUG-2003  
LOCUS 30DGS--08-F02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
DEFINITION sativa cDNA clone 30DGS--08-F02, mRNA sequence.  
ACCESSION CF297446  
VERSION CF297446.1 GI:33666479  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 18)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

# FEATURES

source  
1. .18  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/culturivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="30DGS--08-F02"  
/tissue\_type="leaf"  
/dev\_stages="30 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library I (30DGS)"  
/note="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

Query Match 0.2%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 3.2e+02; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT TTTT 4481  
|||||  
Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 18

# RESULT 892

CF299027 18 bp mRNA linear EST 15-AUG-2003  
LOCUS 7LEAF--02-N14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--02-N14, mRNA sequence.

ACCESSION CF299027  
VERSION CF299027.1 GI:33670788  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 18)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnamh@gbio.com, bhnamh@bio.myongji.ac.kr.

# FEATURES

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Matches 18; Conservative 0;

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Db 1 TTTT TTTT TTTT TTTT TTTT TTTT 18

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LOCUS 7LEAF--03-M14.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
DEFINITION sativa cDNA clone 7LEAF--03-M14, mRNA sequence.

ACCESSION CF299674  
VERSION CF299674.1 GI:33671435  
KEYWORDS EST.  
SOURCE Oryza sativa  
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 18)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

# TITLE

# JOURNAL

CONTACT: Nahm B. H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.myongji.ac.kr.

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Db 1 TTTTTTTTTTTTTTTTTT 18

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RESULT	894
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DEFINITION	7LEAF--06-C12.b1 Rice leaf plasmid cDNA library II ('7LEAF') Oryza
ACCESSION	sativa cDNA clone 7LEAF--06-C12, mRNA sequence.
VERSION	CF301325
KEYWORDS	CF301325.1 GI:33673086
SOURCE	EST.
ORGANISM	Oryza sativa
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REFERENCE	1 (bases 1 to 18)
AUTHORS	Kim, J.-S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
TITLE	Large-scale Sequencing Analysis of Rice ESTs
JOURNAL	Unpublished (2003)
COMMENT	Contact: Nahm B.H.

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taxid: 521321.6355
Email: bhnaahm@bio.com, bhnaahm@bio.myongji.ac.kr.
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Db	1	TTTTTTTTTTTTTTTTTTTT	18						
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DEFINITION		7LEAF--06-L22.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza							
ACCESSION		CF301760							
VERSION		CF301760.1		GI:33673521					
KEYWORDS		EST.							
SOURCE		Oryza sativa							
ORGANISM		Oryza sativa							
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.							
AUTHORS		1 (bases 1 to 18)							
		Kim, S.I., Kim, J.K., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.							
TITLE		Large-scale Sequencing Analysis of Rice ESTs							
JOURNAL		Unpublished (2003)							
COMMENT		Contact: Nahm B.H. Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University Yongin, Kyeonggi, Korea Tel: 82 31 330 6193 Fax: 82 31 321 6355 Email: bhnahm@qsbio.com, bhnahm@bio.myongji.ac.kr.							

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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JOURNAL Unpublished (2003)  
 COMMENT Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Kyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

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Query Match 0.2%; Score 18; DB 1; Length 18;  
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Db 1 CTTTTTTTTTTTTTTT 18

## RESULT 897

CF291665 19 bp mRNA linear EST 14-AUG-2003  
 LOCUS 14ROOT--02-D01.g1 Rice root plasmid cDNA library (14ROOT) Oryza  
 DEFINITION sativa cDNA clone 14ROOT--02-D01, mRNA sequence.

ACCESSION CF291665

VERSION CF291665.1 GI:33660698

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

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Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Db 1 TTTTTTTTTTTTTTTT 18

## RESULT 898

CF293167 19 bp mRNA linear EST 14-AUG-2003  
 LOCUS 30DGS--02-E02.g1 Rice leaf plasmid cDNA library I (30DGS) Oryza  
 DEFINITION sativa cDNA clone 30DGS--02-E02, mRNA sequence.

ACCESSION CF293167

VERSION CF293167.1 GI:33662200

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 19)

AUTHORS Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,

Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.

Large-scale Sequencing Analysis of Rice ESTs

Unpublished (2003)

CONTACT: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division

of Bioscience and Bioinformatics, Myongji University

Yongin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

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Db 2 TTTTTTTTTTTTTTTT 19

## RESULT 899

CF309821 19 bp mRNA linear EST 15-AUG-2003  
 LOCUS ABF--04-C17.g1 ABF3-overexpressing transgenic rice plasmid cDNA  
 DEFINITION library (ABF) Oryza sativa cDNA clone ABF--04-C17, mRNA sequence.

ACCESSION CF309821

VERSION CF309821.1 GI:33681582

KEYWORDS EST.

SOURCE Oryza sativa

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

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REFERENCE
AUTHORS   1 (bases 1 to 19)
           Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
           Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE      Large-scale Sequencing Analysis of Rice ESTs
JOURNAL    Unpublished (2003)
COMMENT    Contact: Nahm B.H.
           Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
           of Bioscience and Bioinformatics, Myongji University
           Yongin, Kyeonggi, Korea
           Tel: 82 31 330 6193
           Fax: 82 31 321 6355
           Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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RESULT 900
LOCUS      CF3311778
DEFINITION ABF--07-D01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
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ACCESSION  CF3311778.1 GI:33683539
VERSION     EST.
KEYWORDS    Oryza sativa
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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REFERENCE   1 (bases 1 to 19)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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DEFINITION ABF--07-D01.g1 ABF3-overexpressing transgenic rice plasmid cDNA
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ACCESSION  CF3311778.1 GI:33683539
VERSION     EST.
KEYWORDS    Oryza sativa
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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then used for PCR. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

Query Match 0.2%; Score 18; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
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ACCESSION  CF331361
VERSION     CF331361.1 GI:33810941
KEYWORDS    EST.
SOURCE      Oryza sativa
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 19)
AUTHORS     Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE       Large-scale Sequencing Analysis of Rice ESTs
JOURNAL     Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.

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RESULT 902
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DEFINITION JMT--04-O17.g1 AtJMT-overexpressing transgenic rice plasmid cDNA
            library (JMT) Oryza sativa cDNA clone JMT--04-O17, mRNA sequence.
ACCESSION  CF335293

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CF335293.1 GI:33818938
EST.
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 19)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
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DB 2 TTTT TTTT TTTT TTTT TTTT 19

RESULT 903
AL587759
LOCUS
DEFINITION
B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
CA853586
B09H12.5, mRNA sequence.
ACCESSION
CA853586
VERSION
CA853586.1 GI:33390391
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 20)
Alkharouf,N.W., Khan,R. and Matthew,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..20
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/mol_type="mRNA"
/cultivar="Peking"
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/clone="B09H12"
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extracted from roots of soybean cv. Peking 12 hrs after
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."
Query Match 0.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
|||||
DB 3 TTTT TTTT TTTT TTTT TTTT 20

RESULT 904
AL587759
LOCUS
DEFINITION
B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
CA853586
B09H12.5, mRNA sequence.
ACCESSION
CA853586
VERSION
CA853586.1 GI:33390391
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 20)
Alkharouf,N.W., Khan,R. and Matthew,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
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/cultivar="Peking"
/db_xref="taxon:3847"
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extracted from roots of soybean cv. Peking 12 hrs after
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."
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Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
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DB 3 TTTT TTTT TTTT TTTT TTTT 20

RESULT 903
AL587759
LOCUS
DEFINITION
B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
CA853586
B09H12.5, mRNA sequence.
ACCESSION
CA853586
VERSION
CA853586.1 GI:33390391
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 20)
Alkharouf,N.W., Khan,R. and Matthew,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..20
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/clone_lib="cDNA Peking library 12hr SCN3"
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infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."
Query Match 0.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
|||||
DB 3 TTTT TTTT TTTT TTTT TTTT 20

RESULT 904
AL587759
LOCUS
DEFINITION
B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
CA853586
B09H12.5, mRNA sequence.
ACCESSION
CA853586
VERSION
CA853586.1 GI:33390391
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 20)
Alkharouf,N.W., Khan,R. and Matthew,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..20
/organism="Glycine max"
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/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from roots of soybean cv. Peking 12 hrs after
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."
Query Match 0.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
|||||
DB 3 TTTT TTTT TTTT TTTT TTTT 20

RESULT 904
AL587759
LOCUS
DEFINITION
B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
CA853586
B09H12.5, mRNA sequence.
ACCESSION
CA853586
VERSION
CA853586.1 GI:33390391
KEYWORDS
EST.
SOURCE
Glycine max (soybean)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 20)
Alkharouf,N.W., Khan,R. and Matthew,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
Location/Qualifiers
1..20
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="B09H12"
/tissue_type="Roots"
/dev_stage="Seedlings"
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/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from roots of soybean cv. Peking 12 hrs after
infection by SCN race 3. These are cloned in pBluescript
SK- phagemid."
Query Match 0.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4464 TTTT TTTT TTTT TTTT TTTT 4481
|||||
DB 3 TTTT TTTT TTTT TTTT TTTT 20

RESULT 904
AL587759
LOCUS
DEFINITION
B09H12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
CA853586
B09H12.5, mRNA sequence.
ACCESSION
CA853586
VERSION
CA853586.1 GI:33390391
KEYWORDS
EST.
SOURCE
Glycine max (soybean
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RESULT 905
CF298207/c
LOCUS
DEFINITION 7LEAF--01-H23.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza
sativa cDNA clone 7LEAF--01-H23, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 20)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhnm@gbio.com, bnhnm@bio.myongji.ac.kr.
FEATURES
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1..20
Location/Qualifiers
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/cultivar="Nackdong"
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/dev_stage="7 days after germination"
/lab_host="E.coli DH10B"
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with oligoribonucleotides and then used as templates for
RT-PCR."
Query Match 0.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4463 CTTTTTTTTTTTTTTTTT 4480
|||||
Db 18 CTTTTTTTTTTTTTTTTT 1

RESULT 906
AZ370699
LOCUS
DEFINITION 1M0121N17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0121N17 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

RESULT 907
AZ849506/c
LOCUS
DEFINITION 2M0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0150P21 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

```

```

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0121 Row: N Column: 17
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
Location/Qualifiers
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/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.2%; Score 18; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4464 TTTTTTTTTTTTTTTTTT 4481
|||||
Db 1 TTTTTTTTTTTTTTTTTT 18

RESULT 907
AZ849506/c
LOCUS
DEFINITION 2M0150P21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC2M0150P21 R, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 20)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center

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/lab host="E. coli strain XL10-Gold, T1-resistant, F-"  
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 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 18; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;  
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RESULT 910  
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 DEFINITION 2M0142B07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC2M0142B07 R, genomic survey sequence.

ACCESSION AZ843648  
 VERSION AZ843648.1 GI:13013556  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 22)  
 AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,F., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
 TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0142 row: B column: 07  
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 High quality sequence stop: 22.

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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 0.2%; Score 18; DB 1; Length 22;  
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Qy 4464 TTTTTTTTTTTTTTTTTT 4481  
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 Db 18 TTTTTTTTTTTTTTTTTT 1

RESULT 911  
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 DEFINITION T. brucei sheared genomic DNA clone 211d06, forward sequence,  
 genomic survey sequence.

ACCESSION AL478564  
 VERSION AL478564.1 GI:11844523  
 KEYWORDS GSS.  
 SOURCE Trypanosoma brucei  
 ORGANISM Trypanosoma brucei  
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
 Trypanosoma.

REFERENCE 1 (bases 1 to 22)  
 AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.B., Rajandream,M.A. and Barrell,B.G.  
 TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh@sanger.ac.uk

COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).  
 Email: nleayed@tigr.org

DETAILS of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T\_brucei/.

FEATURES  
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 Location/Qualifiers

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 Best Local Similarity 100.0%; Pred. No. 5.1e+02;





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DEFINITION	clone UGUC1M0016B10 F, genomic survey sequence.								
ACCESSION	AZ309553								
VERSION	AZ309553.1	G1:10350837							
KEYWORDS	GSS.								
SOURCE	Mus musculus (house mouse)								
ORGANISM	Mus musculus								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 24)								
AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ialam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, 84112, UT								
TITLE									
JOURNAL									
COMMENT	Contact: Robert B. Weiss University of Utah Genome Center Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLCT, 84112, UT Tel.: 801 585 5606 Fax: 801 585 7177 Email: rdunn@genetics.utah.edu Insert length: 10000 Std Error: 0.00 Plate: 0016 row: B column: 10 Seq primer: CGTTGTAAACAGCGCCAGT Class: plasmid ends High quality sequence stop: 24.								
FEATURES	Location/Qualifiers								
source	1..24 /organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="UUGC1M0016B10" /sex="Male" /lab_hosts="E. Coli strain XL10-Gold, Tl-resistant, F-" /clone_lib="Mouse 10kb plasmid UGUC1M library" /notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWP42 (gi 4732114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."								
Query Match	0.2%; Score 18; DB 1; Length 24;								
Best Local Similarity	100.0%; Pred. No. 6.1e+02;								
Matches 18; Conservative	0; Mismatches 0; Indels 0; Gaps 0;								

LOCUS BQ585188 26 bp mRNA linear EST 06-DEC-2002  
 DEFINITION CDNA clone 024-001-E10-SP6 MP1Z-ADIS-024-inflorescence Beta vulgaris  
 ACCESSION BQ585188  
 VERSION BQ585188.1 GI:26114770  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 26)  
 Herwig,R.; Schulz,B.; Weishaar,B.; Hennig,S.; Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 JOURNAL MEDLINE  
 PUBMED 22362189  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 26 Std Error: 0.00  
 Plate: 1 row: E column: 10  
 Seq primer: SP6; CATACGATTAGTGACACTATAG.  
 Location/Qualifiers  
 FEATURES  
 source  
 1..26  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:181514"  
 /db\_xref="taxon:161934"  
 /clone="024-001-E10"  
 /tissue\_type="inflorescence"  
 /lab\_host="EMPH108"  
 /clone\_lib="MP1Z-ADIS-024-inflorescence"  
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGCGCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPB/GABI-Primary database: http://gabi.rzpd.de"

Query Match 0.2%; Score 18; DB 1; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 4463 CTTTTTTTTTTTTTTT 4480  
 Db 7 CTTTTTTTTTTTTTTT 24

RESULT 918  
 AZ465567  
 LOCUS  
 DEFINITION 1M0275C17R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0275C17 R, genomic survey sequence.  
 ACCESSION AZ465567  
 VERSION AZ465567.1 GI:10623788  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

1 (bases 1 to 27)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmood,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0275 row: C column: 17  
 Seq primer: CACACAGGAACACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 27.  
 Location/Qualifiers  
 FEATURES  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0275C17"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 [gil4732114|gb|AF129072.1], a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

FEATURES

Query Match 0.2%; Score 18; DB 1; Length 27;  
 Best Local Similarity 80.8%; Pred. No. 7.8e+02;  
 Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 Oy 2861 AGGAAGCAAGGAGGAGGAGTGGG 2886  
 Db 2 AGGTGGCATGCTGGAGGAGATGGG 27

RESULT 919  
 AZ627840  
 LOCUS  
 DEFINITION 1M0474B05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0474B05 F, genomic survey sequence.  
 ACCESSION AZ627840  
 VERSION AZ627840.1 GI:11750126  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 21)



RESULT 922  
CF300419/c

LOCUS  
DEFINITION

ACCESSION  
VERSION

KEYWORDS  
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CF300419 23 bp mRNA linear EST 15-AUG-2003  
7LEAF--04-M22.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
sativa cDNA clone 7LEAF--04-M22, mRNA sequence.

CF300419  
CF300419.1 GI:33672180  
EST.

Oryza sativa  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 23)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bnhahm@gbio.com, bnhahm@bio.myongji.ac.kr.

FEATURES  
source

1..23  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--04-M22"  
/tissue\_type="leaf"  
/dev\_stages="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/note="Vector: pCR4-TOPO; Site 1: ECORI; mRNA was capped  
with oligoribonucleotides and then used as templates for  
RT-PCR."

Query Match 0.2%; Score 17.8; DB 1; Length 23;  
Best Local Similarity 90.5%; Pred. No. 6e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7407 CAACATCAGCAGCAGCAG 7427

Db 23 CGAGTCAGCAGCAGCAG 3

RESULT 923  
AZ308447/c

LOCUS  
DEFINITION

ACCESSION  
VERSION

KEYWORDS  
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AZ308447 23 bp DNA linear GSS 29-SEP-2000  
1M0011J24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0011J24 F, genomic survey sequence.

AZ308447  
AZ308447.1 GI:10348452  
GSS.

Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 23)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

Contact: Robert B. Weiss  
University of Utah Genome Center

University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0011 row: J column: 24

Seq primer: CGTTGTAACGACGCCAGT

Class: plasmid ends

High quality sequence stop: 23.

FEATURES  
source

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0011J24"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, P-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/note="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 (gi14732114|gb|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 17.8; DB 1; Length 23;  
Best Local Similarity 90.5%; Pred. No. 6e+02;  
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4461 GACCTTTTCTTTTTTTTTTTT 4481

Db 21 GAGTCTTTTTTTTTTTTTTTT 1

RESULT 924  
TA130G11Q

LOCUS  
DEFINITION

ACCESSION  
VERSION

KEYWORDS  
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

TA130G11Q 23 bp DNA linear GSS 13-DEC-2000  
T. brucei sheared genomic DNA clone 130g11, reverse sequence,  
genomic survey sequence.

AL464277

AL464277.1 GI:11834540

GSS.

Trypanosoma brucei

Trypanosoma brucei

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma.

1 (bases 1 to 23)

Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,

Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,

Melville, S.E., Rajadream, M.A. and Barrell, B.G.

Direct Submission

Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing

project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,

Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and

nh@sanger.ac.uk

Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Email: nelsaved@tigr.org

Details of T. brucei sequencing at the Sanger Centre are available at [http://www.sanger.ac.uk/Projects/T\\_brucei/](http://www.sanger.ac.uk/Projects/T_brucei/).

## FEATURES

source

1. .23  
 /organism="Trypanosoma brucei"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:5691"  
 /clone="130g11"

Query Match 0.2%; Score 17.8; DB 1; Length 23;  
 Best Local Similarity 90.5%; Pred. No. 6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3726 CATTCATTGAGCTTTTAAAA 3746

Db 3 CATTTATTGTGCTTTTAAAA 23

## RESULT 925

BX621433/c

LOCUS BX621433 NAPI Anopheles gambiae cDNA clone ANGNP111A03T7, mRNA  
 DEFINITION sequence.

ACCESSION BX621433

VERSION BX621433.1 GI:33542952  
 EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;  
 Anopheles.

REFERENCE 1 (bases 1 to 24)

AUTHORS Lobo,N.L., Gardner,M., Romans,P. and Collins,F.H.

TITLE Anopheles gambiae EST, Center for Tropical Disease Research and

Training

JOURNAL Unpublished (2003)

COMMENT Contact: Frank H. Collins

Center for Tropical Disease Research and Training

University of Notre Dame

Notre Dame, IN 46556, USA

Tel: 574-631-9245

Fax: 574-631-3996

Email: frank.h.collins.75@nd.edu.

## FEATURES

source

1. .24  
 /organism="Anopheles gambiae"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7165"  
 /clone="ANGNP111A03T7"  
 /lab\_host="E. coli DH10B"  
 /clone\_lib="NAPI"

Site 1: NotI;  
 Site 2: EcoRI; ESTs sequenced from the T7 priming site that reads from the 5' end of cDNA. The NAPI is a directionally cloned and normalized, oligo-T primed cDNA library constructed from a mixture of Anopheles gambiae developmental stages according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

Query Match 0.2%; Score 17.8; DB 1; Length 24;  
 Best Local Similarity 90.5%; Pred. No. 6e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7410 CATCAGCAGCAGCAGCAGCAG 7430

Db 22 CGTCAGCAGCAGCAGCAGCAG 2

## RESULT 926

AZ486450

LOCUS

DEFINITION

AZ486450 24 bp DNA linear GSS 05-OCT-2000  
 IM0314A06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

ACCESSION AZ486450

VERSION AZ486450.1 GI:10653235

KEYWORDS GSS.

SOURCE Mus musculus

ORGANISM

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;

REFERENCE 1 (bases 1 to 24)

AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von

Niederhausern,A. and Wright,D., Weiss,R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL plasmid inserts

COMMENT Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0314 row: A column: 06

Seq primer: CACACAGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 24.

FEATURES

source

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/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0314A06"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector DNA was prepared from a derivative

of pWD42 (gil4732114[gb]|AF129072.1), a copy-number

inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into

chemically-competent E. coli XL10-Gold (Stratagene) cells

and selected for ampicillin resistance."

Query Match 0.2%; Score 17.8; DB 1; Length 24;

Best Local Similarity 90.5%; Pred. No. 6.6e+02;

Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 6986 ACAGATGAGTGGGAAAGGG 7006
DB 3 AGAGATGGGTGGGAAAGGG 23

RESULT 927
AZ814559
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 24)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D. Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2010 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0082 row: P column: 18
Seq primer: CGTTGTAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 24.
FEATURES
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1..24
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0082P18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
Query Match 0.2%; Score 17.8; DB 1; Length 24;
Best Local Similarity 90.5%; Pred. No. 6.6e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTTTT 4483

```

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DB 4 CTTTTTTCTTTCTTTTTT 24

RESULT 928
AI445764/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

25 bp mRNA linear EST 13-APR-1999
tj09g10.x1 NCI CGAP Gas4 Homo sapiens cDNA clone IMAGE:2141058 3,
similar to SW:YMO4 PARTE P15605 HYPOTHETICAL 18.8 KD PROTEIN
; contains element L1 repetitive element ;, mRNA sequence.
AI445764
AI445764.1 GI:4290493
EST.
Homo sapiens (human)
Homo sapiens
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 25)
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapps-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Trace considered overall poor quality
Insert Length: 715 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1.
FEATURES
source
1..25
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2141058"
/tissue="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host="DH10B"
/clone_lib="NCI-CCAP Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.69 kb. Life Technologies catalog #:
11549-011"
Query Match 0.2%; Score 17.8; DB 1; Length 25;
Best Local Similarity 90.5%; Pred. No. 7.2e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4463 CTTTTTTTTTTTTTTTTT 4483
DB 22 CTTTTTTGTGTTTTTAAT 2

RESULT 929
BX554728
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

26 bp mRNA linear EST 10-OCT-2003
BX554728 Glossina morsitans morsitans adult infected gut Glossina
morsitans morsitans cDNA clone Tse17b03_plc, mRNA sequence.
BX554728
BX554728.1 GI:33436050
EST.
Glossina morsitans morsitans
Glossina morsitans morsitans
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

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Query Match 0.2%; Score 17.8; DB 1; Length 27;  
 Best Local Similarity 90.5%; Pred. No. 8.4e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4460 GGACATTTTTTTTTTTTTTTT 4480  
 Db 7 GAAGTTTTTTTTTTTTTTTTT 27

## RESULT 932

CF300303 27 bp mRNA linear EST 15-AUG-2003  
 LOCUS 7LEAF--04-K11.b1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 DEFINITION sativa cDNA clone 7LEAF--04-K11, mRNA sequence.

ACCESSION CF300303  
 VERSION CF300303.1 GI:33672064  
 KEYWORDS EST.

## SOURCE

ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)

## TITLE

JOURNAL Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 COMMENT of Bioscience and Bioinformatics, Myongui University  
 Yonjin, Kyeonggi, Korea

Tel: 82 31 330 6193

Fax: 82 31 321 6355

Email: bhnam@bio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

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1..27  
 /organism="Oryza sativa"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:4530"  
 /clone="7LEAF--04-K11"  
 /tissue\_type="leaf"  
 /dev\_stages="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

Query Match 0.2%; Score 17.8; DB 1; Length 27;  
 Best Local Similarity 90.5%; Pred. No. 8.4e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4464 TTTTCTTTTTTTTTTTTTTTT 4484  
 Db 1 TTTTCTTTTTTTTTTTACTTG 21

## RESULT 933

AZ628054 27 bp DNA linear GSS 13-DEC-2000  
 LOCUS 1M0476H19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0476H19 F, genomic survey sequence.

ACCESSION AZ628054  
 VERSION AZ628054.1 GI:11750244  
 KEYWORDS GSS.

## SOURCE

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 27)

## REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## JOURNAL

COMMENT Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: rdunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0476 row: H column: 19

Seq primer: CGTGTAAACGACGGCCAGT

Class: plasmid ends

High quality sequence stop: 27.

## FEATURES

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1..27  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0476H19"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnates/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (gi|4732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

Query Match 0.2%; Score 17.8; DB 1; Length 27;  
 Best Local Similarity 90.5%; Pred. No. 8.4e+02;  
 Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4458 ATGGACTTTTTTTTTTTTTTTT 4478  
 Db 7 ATGTAGTTTTTTTTTTTTTTT 27

## RESULT 934

AZ827060/c 29 bp DNA linear GSS 20-FEB-2001  
 LOCUS 2M0103F17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC2M0103F17 F, genomic survey sequence.

ACCESSION AZ827060  
 VERSION AZ827060.1 GI:12996968  
 KEYWORDS GSS.

## SOURCE

ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 29)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

Reilly,M., Rose,M., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0103 row: F column: 17  
Seq primer: CGTTGTAACAGCGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 29.

# FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0103F17"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 17.8; DB 1; Length 29;  
Best Local Similarity 75.9%; Pred. No. 9.6e+02;  
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAAAACAAAAT 4040  
||||| ||||| ||||| ||||| ||||| |||||  
Db 29 AAAACACAAAAAACAAACAAAAAAAAT 1

RESULT 935  
AZ597046  
LOCUS  
DEFINITION  
AZ597046 31 bp DNA linear GSS 13-DEC-2000  
clone UUGC1M0410K08 R, genomic survey sequence.  
ACCESSION  
AZ597046  
VERSION  
AZ597046.1 GI:11719236  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 31)  
REFERENCE  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Stokes,R., Tingey,A., von

# TITLE

## JOURNAL COMMENT

Niederhausern,A. and Wright,D.,Weiss,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0410 row: K column: 08  
Seq primer: CACACAGGAACAGCTATGACC  
Class: plasmid ends  
High quality sequence stop: 31.

# FEATURES

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0410K08"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, Tl-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

Query Match 0.2%; Score 17.8; DB 1; Length 31;  
Best Local Similarity 75.9%; Pred. No. 1.1e+03;  
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4012 AAAATGAGAAAAAGAGAGAAAAACAAAAT 4040  
||||| ||||| ||||| ||||| ||||| |||||  
Db 3 AAAACACAAAAAACAAACAAAAAAAAT 31

# RESULT 936

## AZ400441

### LOCUS

#### DEFINITION

AZ400441 32 bp DNA linear GSS 03-OCT-2000  
clone UUGC1M0166C14 R, genomic survey sequence.

#### ACCESSION

#### AZ400441

#### VERSION

#### AZ400441.1

#### KEYWORDS

#### GSS.

#### SOURCE

#### Mus musculus

#### (house mouse)

#### ORGANISM

#### Mus musculus

#### Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

#### Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### 1 (bases 1 to 32)

#### REFERENCE

#### Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

#### Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,

#### Reilly,M., Rose,M., Stokes,R., Tingey,A., von

#### Niederhausern,A. and Wright,D.,Weiss,R.

CONTACT: FRAZER MURRAY

```

Db      33 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5

RESULT 939
AL587876/c
LOCUS
DEFINITION AL587876 BP Chicken Brain Library Gallus gallus cDNA clone
            34 bp mRNA linear EST 02-MAR-2001
            ROS064F10, mRNA sequence.
ACCESSION AL587876
VERSION   AL587876.1 GI:13192910
KEYWORDS  EST.
SOURCE    Gallus gallus (chicken)
ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 34)
AUTHORS  Murray,F.
TITLE    BP Chicken Brain Library
JOURNAL  Unpublished (2001)
COMMENT  Contact: Frazer Murray
            Dept. Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UK
            Tel: +44 (0)131 527 4200
            Fax: +44 (0)131 440 0434
            Email: frazer.murray@bbsrc.ac.uk
            GCGGCGCGCTTTTTCCTTTTTCCTTTT 3' Poly A RNA purchased from Clonetechn
            (*6854-
            Seq primer: M13F.
            Location/Qualifiers
            1..34
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            /lab_host="DH10B"
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            unidirectionally. Primer: Oligo dt. 5' adaptor sequence:
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            GCGGCGCGCTTTTTCCTTTTTCCTTTT 3' Poly A RNA purchased from
            Clonetechn (*6854-1)"

Query Match 0.2%; Score 17.6; DB 1; Length 34;
Best Local Similarity 75.9%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db      29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 940
BI094838
LOCUS
DEFINITION EST-CD34N-038 cDNA library of human CD 34+ stem/progenitor cells
            Homo sapiens cDNA 3', mRNA sequence.
ACCESSION BI094838
VERSION   BI094838.1 GI:17737215
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 24)
AUTHORS  Zhou,G., Chen,J., Lee,S., Terry,C., Rowley,J.D. and Wang,S.M.
TITLE    The pattern of gene expression in human hematopoietic CD34+
            stem/progenitor cells
JOURNAL  Unpublished (2001)
COMMENT  Contact: Wang SM

Query Match 0.2%; Score 17.6; DB 1; Length 34;
Best Local Similarity 75.9%; Pred. No. 1.2e+03;
Matches 22; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      4012 AAATGAGAAAAGAGAGAAAACAAAT 4040
        ||||| ||||| ||||| ||||| |||||
Db      29 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 940
BI094838
LOCUS
DEFINITION EST-CD34N-038 cDNA library of human CD 34+ stem/progenitor cells
            Homo sapiens cDNA 3', mRNA sequence.
ACCESSION BI094838
VERSION   BI094838.1 GI:17737215
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 24)
AUTHORS  Zhou,G., Chen,J., Lee,S., Terry,C., Rowley,J.D. and Wang,S.M.
TITLE    The pattern of gene expression in human hematopoietic CD34+
            stem/progenitor cells
JOURNAL  Unpublished (2001)
COMMENT  Contact: Wang SM

FEATURES
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FEATURES
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Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4466 TTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTG 4489
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Db      1 TTTTTCCTTTTTCCTTTTTCCTTTTCGTTTCATG 24

RESULT 941
AZ827015
LOCUS
DEFINITION AZ827015 Mouse 10kb plasmid UUGCIM library Mus musculus genomic
            clone UUGC2M0103J11 F, genomic survey sequence.
ACCESSION AZ827015
VERSION   AZ827015.1 GI:12996923
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0103 row: J column: 11
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
            Location/Qualifiers
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            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0103J11"

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```

Hem/Onc
University of Chicago Medical Center
5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Tel: 773-702-6788
Fax: 773-702-3002
Email: swangl@midway.uchicago.edu
This EST fragment was amplified from cDNA Library of human CD 34+
stem/progenitor cells with GLGI technique (Generation of Longer
cDNA fragments from SAGE tags for Gene Identification, Proc. Natl.
Acad. Sci. USA 97, 349, 2000), which starts from the 3' end till
the first CATG site of the target cDNA sequence.
Seq primer: M13 Forward.
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            /db_xref="taxon:9606"
            /tissue_type="Bone marrow"
            /cell_type="CD34+ stem/progenitor cells"
            /clone_lib="CDNA library of human CD 34+ stem/progenitor
            cells"
            /note="3'ESTs converted from the SAGE tag sequences using
            GLGI method"

Query Match 0.2%; Score 17.6; DB 1; Length 24;
Best Local Similarity 83.3%; Pred. No. 7.1e+02;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      4466 TTTTTCCTTTTTCCTTTTTCCTTTTTCCTTTG 4489
        ||||| ||||| ||||| ||||| |||||
Db      1 TTTTTCCTTTTTCCTTTTTCCTTTTCGTTTCATG 24

RESULT 941
AZ827015
LOCUS
DEFINITION AZ827015 Mouse 10kb plasmid UUGCIM library Mus musculus genomic
            clone UUGC2M0103J11 F, genomic survey sequence.
ACCESSION AZ827015
VERSION   AZ827015.1 GI:12996923
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D., Weiss,R.
TITLE    Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
JOURNAL  Unpublished (2000)
COMMENT  Contact: Robert B. Weiss
            University of Utah Genome Center
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000 Std Error: 0.00
            Plate: 0103 row: J column: 11
            Seq primer: CGTTGTAACGACGCCAGT
            Class: plasmid ends
            High quality sequence stop: 24.
            Location/Qualifiers
            1..24
            /organism="Mus musculus"
            /mol_type="genomic DNA"
            /strain="C57BL/6J"
            /db_xref="taxon:10090"
            /clone="UUGC2M0103J11"

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